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TERMINAL (ENTER 1, 2, 3, OR ?):2

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 NEWS 1   Web Page for STN Seminar Schedule - N. America
 NEWS 2   JAN 02   STN pricing information for 2008 now available
 NEWS 3   JAN 16   CAS patent coverage enhanced to include exemplified
                    prophetic substances
 NEWS 4   JAN 28   USPATFULL, USPAT2, and USPATOLD enhanced with new
                    custom IPC display formats
 NEWS 5   JAN 28   MARPAT searching enhanced
 NEWS 6   JAN 28   USGENE now provides USPTO sequence data within 3 days
                    of publication
 NEWS 7   JAN 28   TOXCENTER enhanced with reloaded MEDLINE segment
 NEWS 8   JAN 28   MEDLINE and LMEDLINE reloaded with enhancements
 NEWS 9   FEB 08   STN Express, Version 8.3, now available
 NEWS 10   FEB 20   PCI now available as a replacement to DPCI
 NEWS 11   FEB 25   IFIREF reloaded with enhancements
 NEWS 12   FEB 25   IMSPRODUCT reloaded with enhancements
 NEWS 13   FEB 29   WPINDEX/WPIDS/WPIX enhanced with ECLA and current
                    U.S. National Patent Classification
 NEWS 14   MAR 31   IFICDB, IFIPAT, and IFIUDB enhanced with new custom
                    IPC display formats
 NEWS 15   MAR 31   CAS REGISTRY enhanced with additional experimental
                    spectra
 NEWS 16   MAR 31   CA/CAplus and CASREACT patent number format for U.S.
                    applications updated
 NEWS 17   MAR 31   LPCI now available as a replacement to LDPCI
 NEWS 18   MAR 31   EMBASE, EMBAL, and LEMBASE reloaded with enhancements
 NEWS 19   APR 04   STN AnaVist, Version 1, to be discontinued
 NEWS 20   APR 15   WPIDS, WPINDEX, and WPIX enhanced with new
                    predefined hit display formats
 NEWS 21   APR 28   EMBASE Controlled Term thesaurus enhanced
 NEWS 22   APR 28   IMSRESEARCH reloaded with enhancements
 NEWS 23   MAY 30   INPAFAMDB now available on STN for patent family
                    searching
 NEWS 24   MAY 30   DGENE, PCTGEN, and USGENE enhanced with new homology
                    sequence search option
 NEWS 25   JUN 06   EPFULL enhanced with 260,000 English abstracts
 NEWS 26   JUN 06   KOREAPAT updated with 41,000 documents
 NEWS 27   JUN 13   USPATFULL and USPAT2 updated with 11-character
                    patent numbers for U.S. applications
 NEWS 28   JUN 19   CAS REGISTRY includes selected substances from
                    web-based collections
 NEWS 29   JUN 25   CA/CAplus and USPAT databases updated with IPC
                    reclassification data
 NEWS 30   JUN 30   AEROSPACE enhanced with more than 1 million U.S.
                    patent records
 NEWS 31   JUN 30   EMBASE, EMBAL, and LEMBASE updated with additional
                    options to display authors and affiliated

organizations
 NEWS 32   JUN 30   STN on the Web enhanced with new STN AnaVist
                    Assistant and BLAST plug-in
 NEWS 33   JUN 30   STN AnaVist enhanced with database content from EPFULL

 NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
              AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

 NEWS HOURS   STN Operating Hours Plus Help Desk Availability
 NEWS LOGIN   Welcome Banner and News Items
 NEWS IPC8   For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that
specific topic.

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* * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 13:55:21 ON 07 JUL 2008

=> index bioscience
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS   SINCE FILE   TOTAL
                                                    ENTRY   SESSION
FULL ESTIMATED COST   0.21   0.21

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
      AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
      CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
      DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:55:47 ON 07 JUL 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view
search error messages that display as 0* with SET DETAIL OFF.

=> s Lactobacillus reuteri and toxin(p)bind? and CD4+ cell? and (food or tablet or
dietary supplement or confectionery or drug)
        0*   FILE ADISCTI

=> s Lactobacillus reuteri and toxin(p)bind? and CD4+ cells
        0*   FILE ADISCTI

=> s Lactobacillus reuteri and toxin(p)bind?
        0*   FILE ADISNEWS
        0*   FILE ANTE
        0*   FILE AQUALINE
        0*   FILE BIOENG
        1*   FILE BIOTECHABS
        1*   FILE BIOTECHDS
        0*   FILE BIOTECHNO
        2   FILE CAPLUS
        0*   FILE CEABA-VTB
        0*   FILE CIN
  27 FILES SEARCHED...
        0*   FILE ESBIOBASE
        0*   FILE FOMAD

```
            0*   FILE FOREGE
            2*   FILE FROSTI
            0*   FILE FSTA
            5    FILE GENBANK
            1    FILE IFIPAT
            0*   FILE KOSMET
            0*   FILE NTIS
            0*   FILE NUTRACEUT
            1*   FILE PASCAL
            0*   FILE PHARMAML
            1    FILE SCISEARCH
            1    FILE TOXCENTER
   60 FILES SEARCHED...
           21    FILE USPATFULL
            3    FILE USPAT2
            0*   FILE WATER
            2    FILE WPIDS
            2    FILE WPINDEX
```

   13 FILES HAVE ONE OR MORE ANSWERS,   69 FILES SEARCHED IN STNINDEX

L1   QUE LACTOBACILLUS REUTERI AND TOXIN(P) BIND?

=> file biotechds biotechabs caplus frosti genbank ifipat pascal scisearch
toxcenter uspatfull uspat2

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	3.90	4.11

FILE 'BIOTECHDS' ENTERED AT 13:59:37 ON 07 JUL 2008
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FILE 'BIOTECHABS' ACCESS NOT AUTHORIZED

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FILE 'GENBANK' ENTERED AT 13:59:37 ON 07 JUL 2008

FILE 'IFIPAT' ENTERED AT 13:59:37 ON 07 JUL 2008
COPYRIGHT (C) 2008 IFI CLAIMS(R) Patent Services (IFI)

FILE 'PASCAL' ENTERED AT 13:59:37 ON 07 JUL 2008
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FILE 'TOXCENTER' ENTERED AT 13:59:37 ON 07 JUL 2008
COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPATFULL' ENTERED AT 13:59:37 ON 07 JUL 2008
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

```
FILE 'USPAT2' ENTERED AT 13:59:37 ON 07 JUL 2008
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

=> s l1
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'TOXIN(P) BIND?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'TOXIN(P) BIND?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'TOXIN(P) BIND?'
L2          38 L1

=> rem dup l2
DUP IS NOT VALID HERE
The DELETE command is used to remove various items stored by the
system.

To delete a saved query, saved answer set, saved L-number list, SDI
request, batch request, mailing list, or user-defined cluster, format,
or search field, enter the name.  The name may include ?  for left,
right, or simultaneous left and right truncation.

Examples:

  DELETE BIO?/Q          - delete query names starting with BIO
  DELETE ?DRUG/A         - delete answer set names ending with DRUG
  DELETE ?ELEC?/L        - delete L-number lists containing ELEC
  DELETE ANTICOAG/S      - delete SDI request
  DELETE ENZYME/B        - delete batch request
  DELETE .MYCLUSTER      - delete user-defined cluster
  DELETE .MYFORMAT       - delete user-defined display format
  DELETE .MYFIELD        - delete user-defined search field
  DELETE NAMELIST MYLIST - delete mailing list

To delete an ordered document or an offline print, enter its
number.

Examples:

  DELETE P123001C        - delete print request
  DELETE D134002C        - delete document order request

To delete an individual L-number or range of L-numbers, enter the
L-number or L-number range.  You may also enter DELETE LAST followed
by a number, n, to delete the last n L-numbers.  RENUMBER or
NORENUMBER may also be explicitly specified to override the value of
SET RENUMBER.

Examples:

  DELETE L21             - delete a single L-number
  DELETE L3-L6           - delete a range of L-numbers
  DELETE LAST 4          - delete the last 4 L-numbers
  DELETE L33-            - delete L33 and any higher L-number
  DELETE -L55            - delete L55 and any lower L-number
  DELETE L2-L6 RENUMBER - delete a range of L-numbers and
                           renumber remaining L-numbers
  DELETE RENUMBER        - renumber L-numbers after deletion of
                           intermediate L-numbers

Entire sets of saved items, SDI requests, batch requests, user-defined
items, or E-numbers can be deleted.
```

Examples:

```
DELETE SAVED/Q - delete all saved queries
DELETE SAVED/A - delete all saved answer sets
DELETE SAVED/L - delete all saved L-number lists
DELETE SAVED   - delete all saved queries, answer sets,
                 and L-number lists
DELETE SAVED/S - delete all SDI requests
DELETE SAVED/B - delete all batch requests
DELETE CLUSTER - delete all user-defined clusters
DELETE FORMAT  - delete all user-defined display formats
DELETE FIELD   - delete all user-defined search fields
DELETE SELECT  - delete all E-numbers
DELETE HISTORY - delete all L-numbers and restart the
                 session at L1
```

To delete an entire multifile SDI request, enter DELETE and
the name of the request. To delete a component from the
multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l2
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L2
L3            34 DUP REM L2 (4 DUPLICATES REMOVED)

=> s l3 and (tablet or food or dietary suplement or confectionery or drug) and
product
L4            27 L3 AND (TABLET OR FOOD OR DIETARY SUPLEMENT OR CONFECTIONERY
                 OR DRUG) AND PRODUCT

=> rem dup l4
DUP IS NOT VALID HERE
```
The DELETE command is used to remove various items stored by the
system.

To delete a saved query, saved answer set, saved L-number list, SDI
request, batch request, mailing list, or user-defined cluster, format,
or search field, enter the name. The name may include ? for left,
right, or simultaneous left and right truncation.

Examples:

```
DELETE BIO?/Q           - delete query names starting with BIO
DELETE ?DRUG/A          - delete answer set names ending with DRUG
DELETE ?ELEC?/L         - delete L-number lists containing ELEC
DELETE ANTICOAG/S       - delete SDI request
DELETE ENZYME/B         - delete batch request
DELETE .MYCLUSTER       - delete user-defined cluster
DELETE .MYFORMAT        - delete user-defined display format
DELETE .MYFIELD         - delete user-defined search field
DELETE NAMELIST MYLIST - delete mailing list
```

To delete an ordered document or an offline print, enter its
number.

Examples:

```
DELETE P123001C         - delete print request
DELETE D134002C         - delete document order request
```

To delete an individual L-number or range of L-numbers, enter the
L-number or L-number range. You may also enter DELETE LAST followed
by a number, n, to delete the last n L-numbers. RENUMBER or
NORENUMBER may also be explicitly specified to override the value of
SET RENUMBER.

Examples:

```
  DELETE L21           - delete a single L-number
  DELETE L3-L6         - delete a range of L-numbers
  DELETE LAST 4        - delete the last 4 L-numbers
  DELETE L33-          - delete L33 and any higher L-number
  DELETE -L55          - delete L55 and any lower L-number
  DELETE L2-L6 RENUMBER - delete a range of L-numbers and
                         renumber remaining L-numbers
  DELETE RENUMBER      - renumber L-numbers after deletion of
                         intermediate L-numbers
```

Entire sets of saved items, SDI requests, batch requests, user-defined
items, or E-numbers can be deleted.

Examples:

```
  DELETE SAVED/Q - delete all saved queries
  DELETE SAVED/A - delete all saved answer sets
  DELETE SAVED/L - delete all saved L-number lists
  DELETE SAVED   - delete all saved queries, answer sets,
                   and L-number lists
  DELETE SAVED/S - delete all SDI requests
  DELETE SAVED/B - delete all batch requests
  DELETE CLUSTER - delete all user-defined clusters
  DELETE FORMAT  - delete all user-defined display formats
  DELETE FIELD   - delete all user-defined search fields
  DELETE SELECT  - delete all E-numbers
  DELETE HISTORY - delete all L-numbers and restart the
                   session at L1
```

To delete an entire multifile SDI request, enter DELETE and
the name of the request. To delete a component from the
multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l4
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L4
L5              27 DUP REM L4 (0 DUPLICATES REMOVED)

=> d l5 1-27

L5   ANSWER 1 OF 27  USPATFULL on STN
AN     2007:296111  USPATFULL
TI     Lactobacillus acidophillus nucleic acid sequences encoding cell surface
       protein homologues and uses therefore
IN     Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
       Altermann, Eric, Palmerston North, NEW ZEALAND
       Buck, B. Logan, Banner Elk, NC, UNITED STATES
       Russell, W. Michael, Newburgh, IN, UNITED STATES
PA     North Carolina State University, Raleigh, NC, UNITED STATES (U.S.
       corporation)
PI     US 20070258955     A1  20071108
AI     US 2007-701335     A1  20070201 (11)
RLI    Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING
```

```
PRAI    US 2003-465621P      20030425 (60)
DT      Utility
FS      APPLICATION
LN.CNT 5104
INCL    INCLM: 424/093.400
        INCLS: 435/252.100; 435/252.900; 435/320.100; 435/006.000; 435/007.100;
               435/070.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100
NCL     NCLM: 424/093.400
        NCLS: 435/006.000; 435/007.100; 435/070.100; 435/252.100; 435/252.900;
              435/320.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100
IC      IPCI   A61K0035-00 [I,A]; A61K0038-00 [I,A]; A61P0001-00 [I,A];
               C07H0021-02 [I,A]; C07H0021-00 [I,C*]; C07K0016-00 [I,A];
               C07K0004-00 [I,A]; C12N0001-20 [I,A]; C12N0015-00 [I,A];
               C12P0021-04 [I,A]; C12Q0001-68 [I,A]
        IPCR   A61K0035-00 [I,C]; A61K0035-00 [I,A]; A61K0038-00 [I,C];
               A61K0038-00 [I,A]; A61P0001-00 [I,C]; A61P0001-00 [I,A];
               C07H0021-00 [I,C]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
               C07K0004-00 [I,C]; C07K0004-00 [I,A]; C07K0014-195 [I,C*];
               C07K0014-335 [I,A]; C07K0016-00 [I,C]; C07K0016-00 [I,A];
               C12N0001-20 [I,C]; C12N0001-20 [I,A]; C12N0001-21 [I,C*];
               C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
               C12N0015-00 [I,C]; C12N0015-00 [I,A]; C12P0021-04 [I,C];
               C12P0021-04 [I,A]; C12P0021-06 [I,C*]; C12P0021-06 [I,A];
               C12Q0001-68 [I,C]; C12Q0001-68 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5   ANSWER 2 OF 27  USPATFULL on STN
AN      2007:197155  USPATFULL
TI      Lactobacillus acidophilus nucleic acid sequences encoding cell surface
        protein homologues and uses therefore
IN      Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
        Altermann, Eric, Palmerston North, NEW ZEALAND
        Buck, B. Logan, Banner Elk, NC, UNITED STATES
        Russell, W. Michael, Newburgh, IN, UNITED STATES
PA      North Carolina State University, Raleigh, NC, UNITED STATES, 27695-8210
        (U.S. corporation)
PI      US 20070172495      A1  20070726
AI      US 2007-701319      A1  20070201 (11)
RLI     Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING
PRAI    US 2003-465621P      20030425 (60)
DT      Utility
FS      APPLICATION
LN.CNT 5104
INCL    INCLM: 424/234.100
        INCLS: 514/044.000; 435/006.000; 435/007.320; 435/069.100; 435/252.900;
               435/471.000; 530/350.000; 536/023.700
NCL     NCLM: 424/234.100
        NCLS: 435/006.000; 435/007.320; 435/069.100; 435/252.900; 435/471.000;
              514/044.000; 530/350.000; 536/023.700
IC      IPCI   A61K0048-00 [I,A]; A61K0039-02 [I,A]; C12Q0001-68 [I,A];
               G01N0033-554 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C*];
               C12P0021-06 [I,A]; C07K0014-335 [I,A]; C07K0014-195 [I,C*]
        IPCR   A61K0048-00 [I,C]; A61K0048-00 [I,A]; A61K0039-02 [I,C];
               A61K0039-02 [I,A]; C07H0021-00 [I,C]; C07H0021-04 [I,A];
               C07K0014-195 [I,C]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
               C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
               C12P0021-06 [I,C]; C12P0021-06 [I,A]; C12Q0001-68 [I,C];
               C12Q0001-68 [I,A]; G01N0033-554 [I,C]; G01N0033-554 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5   ANSWER 3 OF 27  USPATFULL on STN
AN      2007:140436  USPATFULL
```

```
TI      Delivery of trefoil peptides
IN      Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
        Steidler, Lothar, Lokeren, BELGIUM
        Remaut, Erik Rene, Lovendegem, BELGIUM
PI      US 20070122427    A1  20070531
AI      US 2007-654879    A1  20070118 (11)
RLI     Division of Ser. No. US 2002-30390, filed on 16 Apr 2002, PENDING A 371
        of International Ser. No. WO 2000-EP6343, filed on 5 Jul 2000
PRAI    EP 1999-870143    19990705
DT      Utility
FS      APPLICATION
LN.CNT 1335
INCL    INCLM: 424/200.100
        INCLS: 435/252.300; 435/252.900
NCL     NCLM:  424/200.100
        NCLS:  435/252.300; 435/252.900
IC      IPCI   A61K0039-02 [I,A]; C12N0001-21 [I,A]
        IPCR   A61K0039-02 [I,C]; A61K0039-02 [I,A]; C12N0001-21 [I,C];
               C12N0001-21 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5   ANSWER 4 OF 27  USPATFULL on STN
AN      2007:134502  USPATFULL
TI      Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN      Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
        Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
        Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
        Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
        Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA      BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
        (non-U.S. corporation)
PI      US 20070117183    A1  20070524
AI      US 2006-511140    A1  20060828 (11)
RLI     Division of Ser. No. US 2005-55822, filed on 11 Feb 2005, PENDING
        Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED
PRAI    DE 1999-19932125    19990709
        DE 1999-19932227    19990709
        DE 1999-19932228    19990709
        DE 1999-19932230    19990709
        DE 1999-19933005    19990714
        DE 1999-19933006    19990714
        DE 1999-19940764    19990827
        DE 1999-19940766    19990827
        DE 1999-19940832    19990827
        DE 1999-19941378    19990831
        DE 1999-19941379    19990831
        DE 1999-19942077    19990903
        DE 1999-19942079    19990903
        DE 1999-19931418    19990708
        DE 1999-19932126    19990709
        DE 1999-19932229    19990709
        DE 1999-19941396    19990831
        DE 1999-19942087    19990903
        DE 1999-19930476    19990701
        DE 1999-19931419    19990708
        DE 1999-19931420    19990708
        DE 1999-19932206    19990709
        DE 1999-19942088    19990903
        DE 1999-19942124    19990903
        DE 1999-19932928    19990714
        DE 1999-19931415    19990708
        DE 1999-19931424    19990708
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            DE 1999-19931634      19990708
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            DE 1999-19932922      19990714
            DE 1999-19932926      19990714
            DE 1999-19933004      19990714
            DE 1999-19940765      19990827
            DE 1999-19941380      19990831
            DE 1999-19941394      19990831
            DE 1999-19942076      19990903
            DE 1999-19942086      19990903
            DE 1999-19942095      19990903
            DE 1999-19942129      19990903
            US 1999-141031P       19990625 (60)
            US 1999-142101P       19990702 (60)
            US 1999-148613P       19990812 (60)
            US 2000-187970P       20000309 (60)
DT      Utility
FS      APPLICATION
LN.CNT 8386
INCL    INCLM: 435/069.100
        INCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;
               536/023.200
NCL     NCLM:  435/069.100
        NCLS:  435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;
               536/023.200
IC      IPCI   C07H0021-04 [I,A]; C07H0021-00 [I,C*]; C12P0021-06 [I,A];
               C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
               C12N0009-10 [I,A]; C12N0015-74 [I,A]; C12N0001-21 [I,A]
        IPCR   C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C];
               C12N0001-21 [I,A]; C12N0009-10 [I,C]; C12N0009-10 [I,A];
               C12N0015-74 [I,C]; C12N0015-74 [I,A]; C12P0013-00 [I,C];
               C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0021-06 [I,C];
               C12P0021-06 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5      ANSWER 5 OF 27  USPATFULL on STN
AN      2007:127377  USPATFULL
TI      Delivery of trefoil peptides
IN      Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
        Steidler, Lothar, Lokeren, BELGIUM
        Remaut, Erik Rene, Lovendegem, BELGIUM
PI      US 20070110723      A1  20070517
AI      US 2007-654985      A1  20070118 (11)
RLI     Continuation of Ser. No. US 2002-30390, filed on 16 Apr 2002, PENDING A
        371 of International Ser. No. WO 2000-EP6343, filed on 5 Jul 2000
PRAI    EP 1999-870143      19990705
DT      Utility
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FS      APPLICATION
LN.CNT 1328
INCL    INCLM: 424/093.200
        INCLS: 424/093.450
NCL     NCLM:  424/093.200
        NCLS:  424/093.450
IC      IPCI   A61K0048-00 [I,A]
        IPCR   A61K0048-00 [I,C]; A61K0048-00 [I,A]; C12N0015-09 [I,C*];
               C12N0015-09 [I,A]; A61K0035-66 [I,C*]; A61K0035-74 [I,A];
               A61K0038-00 [I,C*]; A61K0038-00 [I,A]; A61P0001-00 [I,C*];
               A61P0001-04 [I,A]; C07K0014-435 [I,C*]; C07K0014-575 [I,A];
               C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0015-16 [I,C*];
               C12N0015-16 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
               C12R0001-01 [N,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5    ANSWER 6 OF 27  USPATFULL on STN
AN      2007:130427  USPATFULL
TI      Delivery of trefoil peptides
IN      Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
        Steidler, Lothar, Lokeren, BELGIUM
        Remaut, Erik Rene, Lonendegem, BELGIUM
PA      Vlaams Interuniversitair Instituut voor Biotechnologie, BELGIUM
        (non-U.S. corporation)
PI      US 7220418       B1  20070522
        WO 2001002570  20010111
AI      US 2000-30390          20000705 (10)
        WO 2000-EP6343         20000705
                               20020416  PCT 371 date
PRAI    EP 1999-870143     19990705
DT      Utility
FS      GRANTED
LN.CNT 1334
INCL    INCLM: 424/200.100
        INCLS: 424/093.450; 424/093.200; 424/234.100; 424/192.100; 514/925.000
NCL     NCLM:  424/200.100
        NCLS:  424/093.200; 424/093.450; 424/192.100; 424/234.100; 514/925.000
IC      IPCI   A01N0063-00 [I,A]; A61K0039-02 [I,A]; A61K0039-00 [I,A]
        IPCR   A01N0063-00 [I,C]; A01N0063-00 [I,A]; C12N0015-09 [I,C*];
               C12N0015-09 [I,A]; A61K0035-66 [I,C*]; A61K0035-74 [I,A];
               A61K0038-00 [I,C*]; A61K0038-00 [I,A]; A61K0039-00 [I,C];
               A61K0039-00 [I,A]; A61K0039-02 [I,C]; A61K0039-02 [I,A];
               A61K0048-00 [I,C*]; A61K0048-00 [I,A]; A61P0001-00 [I,C*];
               A61P0001-04 [I,A]; C07K0014-435 [I,C*]; C07K0014-575 [I,A];
               C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0015-16 [I,C*];
               C12N0015-16 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
               C12R0001-01 [N,A]
EXF     424/200.1; 424/192.1; 424/184.1; 424/234.1; 424/244.1; 424/246.1;
        424/93.2; 424/93.45; 514/2; 514/925; 435/69.3; 435/69.1; 435/71.1;
        435/252.9
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5    ANSWER 7 OF 27  IFIPAT  COPYRIGHT 2008 IFI on STN
AN      11053905  IFIPAT;IFIUDB;IFICDB
TI      METHOD OF IMPROVING IMMUNE FUNCTION IN MAMALS USING LACTOBACILLUS
        REUTERI STRAINS
IN      Kang Ho-Jin (KR); Kwon Ik-boo (KR); Lee Dong-Seog (KR); Mollstam Bo (SE)
PA      Unassigned Or Assigned To Individual (68000)
PI      US 2006002907  A1  20060105
AI      US 2002-531651     20021018
        WO 2002-SE1903     20021018
                           20050415  PCT 371 date
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FI   US 2006002907   20060105
DT   Utility; Patent Application – First Publication
FS   CHEMICAL
      APPLICATION
ED   Entered STN: 9 Jan 2006
      Last Updated on STN: 9 Jan 2006
CLMN 9
GI   1 Figure(s).
      FIG. 1. Confirmation of inhibitory ability against the binding of vero
      cytotoxin(VT) and Gb3 receptor in a culture supernatant of L. reuteri
      through competitive ELISA. Each reacted as follows, on plates coated with
      Gb3, followed by performing ELISA using mAb against VT.

L5   ANSWER 8 OF 27 USPATFULL on STN
AN   2006:274450 USPATFULL
TI   Gene products differentially expressed in cancerous cells
IN   Scott, Elizabeth M., Emeryville, CA, UNITED STATES
      Lamson, George, Emeryville, CA, UNITED STATES
      Kassam, Altaf, Emeryville, CA, UNITED STATES
      Zhang, Guozhong, Emeryville, CA, UNITED STATES
      Sakamoto, Doreen, Emeryville, CA, UNITED STATES
      Garcia, Pablo Dominguez, Emeryville, CA, UNITED STATES
      May, Theresa, Emeryville, CA, UNITED STATES
      Kennedy, Giulia C., Emeryville, CA, UNITED STATES
      Kang, Sanmao, Emeryville, CA, UNITED STATES
      Reinhard, Christoph, Emeryville, CA, UNITED STATES
      Jefferson, Ann Bennett, Emeryville, CA, UNITED STATES
PA   Chiron Corporation (U.S. corporation)
PI   US 20060234246   A1 20061019
AI   US 2004-934842   A1 20040902 (10)
RLI   Continuation-in-part of Ser. No. US 2002-165835, filed on 6 Jun 2002,
      ABANDONED Continuation of Ser. No. US 2000-490818, filed on 25 Jan 2000,
      GRANTED, Pat. No. US 6429302 Continuation-in-part of Ser. No. US
      2001-883152, filed on 15 Jun 2001, ABANDONED Continuation-in-part of
      Ser. No. WO 2003-US15465, filed on 16 May 2003, PENDING
PRAI US 1999-118302P   19990202 (60)
      US 2000-211835P   20000615 (60)
      US 2003-445222P   20030204 (60)
      US 2002-381533P   20020517 (60)
DT   Utility
FS   APPLICATION
LN.CNT 17024
INCL INCLM: 435/006.000
      INCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;
             530/388.800; 536/023.500
NCL   NCLM: 435/006.000
      NCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;
             530/388.800; 536/023.500
IC   IPCI C12Q0001-68 [I,A]; G01N0033-574 [I,A]; C07H0021-04 [I,A];
            C07H0021-00 [I,C*]; C12P0021-06 [I,A]; C07K0014-82 [I,A];
            C07K0016-30 [I,A]; C07K0016-18 [I,C*]
      IPCR C12Q0001-68 [I,C]; C12Q0001-68 [I,A]; C07H0021-00 [I,C];
            C07H0021-04 [I,A]; C07K0014-82 [I,C]; C07K0014-82 [I,A];
            C07K0016-18 [I,C]; C07K0016-30 [I,A]; C12P0021-06 [I,C];
            C12P0021-06 [I,A]; G01N0033-574 [I,C]; G01N0033-574 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5   ANSWER 9 OF 27 USPATFULL on STN
AN   2006:98984 USPATFULL
TI   Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN   Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF

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        Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
        Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
        Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
        Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA      BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
        (non-U.S. corporation)
PI      US 20060084152      A1  20060420
AI      US 2005-239674      A1  20050928 (11)
RLI     Continuation of Ser. No. US 2000-746660, filed on 22 Dec 2000, ABANDONED
        Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
        ABANDONED Continuation-in-part of Ser. No. US 2000-603124, filed on 23
        Jun 2000, ABANDONED
PRAI    DE 1999-19932125     19990709
        DE 1999-19932227     19990709
        DE 1999-19932228     19990709
        DE 1999-19932230     19990709
        DE 1999-19933005     19990714
        DE 1999-19933006     19990714
        DE 1999-19940764     19990827
        DE 1999-19940766     19990827
        DE 1999-19940832     19990827
        DE 1999-19941378     19990831
        DE 1999-19941379     19990831
        DE 1999-19942077     19990903
        DE 1999-19942079     19990903
        DE 1999-19931418     19990708
        DE 1999-19932126     19990709
        DE 1999-19932229     19990709
        DE 1999-19941396     19990831
        DE 1999-19942087     19990903
        DE 1999-19930476     19990701
        DE 1999-19931419     19990708
        DE 1999-19931420     19990708
        DE 1999-19932206     19990709
        DE 1999-19942088     19990903
        DE 1999-19942124     19990903
        DE 1999-19932928     19990714
        DE 1999-19931415     19990708
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        DE 1999-19931435     19990708
        DE 1999-19931443     19990708
        DE 1999-19931453     19990708
        DE 1999-19931457     19990708
        DE 1999-19931465     19990708
        DE 1999-19931478     19990708
        DE 1999-19931510     19990708
        DE 1999-19931541     19990708
        DE 1999-19931573     19990708
        DE 1999-19931592     19990708
        DE 1999-19931632     19990708
        DE 1999-19931634     19990708
        DE 1999-19931636     19990708
        DE 1999-19932130     19990708
        DE 1999-19932186     19990709
        DE 1999-19932922     19990714
        DE 1999-19932926     19990714
        DE 1999-19933004     19990714
        DE 1999-19940765     19990827
        DE 1999-19941380     19990831
        DE 1999-19941394     19990831
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          DE 1999-19942086     19990903
          DE 1999-19942095     19990903
          DE 1999-19942129     19990903
          DE 1999-19932124     19990709
          DE 1999-19932127     19990709
          DE 1999-19932133     19990709
          DE 1999-19932207     19990709
          DE 1999-19932208     19990709
          DE 1999-19932225     19990709
          DE 1999-19932914     19990709
          DE 1999-19940768     19990827
          DE 1999-19940831     19990827
          DE 1999-19941385     19990831
          US 1999-141031P      19990625 (60)
          US 1999-142101P      19990702 (60)
          US 1999-148613P      19990812 (60)
          US 2000-187970P      20000309 (60)
          US 1999-141031P      19990625 (60)
          US 1999-143694P      19990714 (60)
          US 1999-151778P      19990831 (60)
DT        Utility
FS        APPLICATION
LN.CNT    14822
INCL      INCLM: 435/113.000
          INCLS: 435/115.000; 435/252.300
NCL       NCLM:  435/113.000
          NCLS:  435/115.000; 435/252.300
IC        IPCI   C12P0013-12 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
                 C12N0001-20 [I,A]
          IPCR   C12P0013-00 [I,C]; C12P0013-12 [I,A]; C12N0001-20 [I,C];
                 C12N0001-20 [I,A]; C12P0013-08 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5    ANSWER 10 OF 27   USPATFULL on STN
AN        2006:211028  USPATFULL
TI        Nucleic acid sequences relating to Bacteroides fragilis for diagnostics
          and therapeutics
IN        Breton, Gary L., Marlboro, MA, UNITED STATES
PA        Oscient Pharmaceuticals Corporation, Waltham, MA, UNITED STATES (U.S.
          corporation)
PI        US 7090973        B1  20060815
AI        US 2000-540209        20000404 (9)
PRAI      US 1999-128705P   19990409 (60)
DT        Utility
FS        GRANTED
LN.CNT    38850
INCL      INCLM: 435/006.000
          INCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330
NCL       NCLM:  435/006.000
          NCLS:  435/091.200; 536/023.500; 536/024.310; 536/024.330
IC        IPCI   C12Q0001-68 [I,A]; C12P0019-34 [I,A]; C12P0019-00 [I,C*];
                 C07H0021-02 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C*]
EXF       435/91.1; 435/91.2; 435/6; 435/320.1; 435/325; 435/352.3; 536/23.1;
          536/24.1; 536/23.7; 536/24.32; 536/24.3; 514/44
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5    ANSWER 11 OF 27   USPATFULL on STN
AN        2006:146715  USPATFULL
TI        Nucleic acid and amino acid sequences relating to Staphylococcus
          epidermidis for diagnostics and therapeutics
IN        Doucette-Stamm, Lynn, Framingham, MA, UNITED STATES
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          Bush, David, Somerville, MA, UNITED STATES
PA        Wyeth, Madison, NJ, UNITED STATES (U.S. corporation)
PI        US 7060458         B1   20060613
AI        US 1999-450969           19991129 (9)
RLI       Continuation-in-part of Ser. No. US 1998-134001, filed on 13 Aug 1998,
          Pat. No. US 6380370, issued on 30 Apr 2002
PRAI      US 1997-64964P     19971108 (60)
          US 1997-55779P     19970814 (60)
DT        Utility
FS        GRANTED
LN.CNT 35708
INCL      INCLM: 435/069.100
          INCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320
NCL       NCLM:  435/069.100
          NCLS:  435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320
IC        IPCI   C07H0021-04 [I,A]; C07H0021-00 [I,C*]
          IPCR   C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C*];
                 C12N0001-21 [I,A]; C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]
EXF       435/6; 435/91.2; 435/69.1; 536/22.1; 536/23.1; 536/24.3
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5   ANSWER 12 OF 27  USPATFULL on STN
AN        2005:299042  USPATFULL
TI        Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN        Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
          Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
          Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
          Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
          Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA        BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
          (non-U.S. corporation)
PI        US 20050260707     A1   20051124
AI        US 2005-55822      A1   20050211 (11)
RLI       Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED
PRAI      DE 1999-19932125   19990709
          DE 1999-19932227   19990709
          DE 1999-19932228   19990709
          DE 1999-19932230   19990709
          DE 1999-19933005   19990714
          DE 1999-19933006   19990714
          DE 1999-19940764   19990827
          DE 1999-19940766   19990827
          DE 1999-19940832   19990827
          DE 1999-19941378   19990831
          DE 1999-19941379   19990831
          DE 1999-19942077   19990903
          DE 1999-19942079   19990903
          DE 1999-19931418   19990708
          DE 1999-19932126   19990709
          DE 1999-19932229   19990709
          DE 1999-19941396   19990831
          DE 1999-19942087   19990903
          DE 1999-19930476   19990701
          DE 1999-19931419   19990708
          DE 1999-19931420   19990708
          DE 1999-19932206   19990709
          DE 1999-19942088   19990903
          DE 1999-19942124   19990903
          DE 1999-19932928   19990714
          DE 1999-19931415   19990708
          DE 1999-19931424   19990708
          DE 1999-19931428   19990708
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         DE 1999-19931443      19990708
         DE 1999-19931453      19990708
         DE 1999-19931457      19990708
         DE 1999-19931465      19990708
         DE 1999-19931478      19990708
         DE 1999-19931510      19990708
         DE 1999-109931541     19990708
         DE 1999-19931573      19990708
         DE 1999-19931592      19990708
         DE 1999-19931632      19990708
         DE 1999-19931634      19990708
         DE 1999-19931636      19990708
         DE 1999-19932130      19990708
         DE 1999-19932186      19990709
         DE 1999-19932922      19990714
         DE 1999-19932926      19990714
         DE 1999-19933004      19990714
         DE 1999-19940765      19990827
         DE 1999-19941380      19990831
         DE 1999-19941394      19990831
         DE 1999-19942076      19990903
         DE 1999-19942086      19990903
         DE 1999-19942095      19990903
         DE 1999-19942129      19990903
         US 1999-141031P       19990625 (60)
         US 1999-142101P       19990702 (60)
         US 1999-148613P       19990812 (60)
         US 2000-187970P       20000309 (60)
DT       Utility
FS       APPLICATION
LN.CNT 8777
INCL     INCLM: 435/069.100
         INCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200
NCL      NCLM:  435/069.100
         NCLS:  435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200
IC       [7]
         ICM    C12P021-06
         ICS    C12P013-04; C07H021-04; C12N001-20; C12N015-74; C12N009-10
         IPCI   C12P0021-06 [ICM,7]; C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C*];
                C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]; C12N0001-20 [ICS,7];
                C12N0015-74 [ICS,7]; C12N0009-10 [ICS,7]
         IPCR   C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
                C07K0014-34 [I,A]; C12N0001-20 [I,C*]; C12N0001-20 [I,A];
                C12N0009-00 [I,C*]; C12N0009-00 [I,A]; C12N0009-10 [I,C*];
                C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
                C12P0013-00 [I,C*]; C12P0013-04 [I,A]; C12P0021-06 [I,C*];
                C12P0021-06 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5   ANSWER 13 OF 27  USPATFULL on STN
AN       2005:268092  USPATFULL
TI       Modified bacterial surface layer proteins
IN       Pouwels, Pieter Hendrik, Rijswijk, NETHERLANDS
         Smit, Egbert, Sittard, NETHERLANDS
         Tielen, Frans, Prinsenbeek, NETHERLANDS
PI       US 20050233408     A1  20051020
AI       US 2003-500307     A1  20021223 (10)
         WO 2002-EP14749        20021223
                                20041122  PCT 371 date
PRAI     EP 2001-310937     20011228
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DT      Utility
FS      APPLICATION
LN.CNT 2664
INCL    INCLM: 435/034.000
        INCLS: 530/395.000; 435/252.300
NCL     NCLM:  435/034.000
        NCLS:  435/252.300; 530/395.000
IC      [7]
        ICM     C12Q001-04
        ICS     C12N001-21; C07K014-335
        IPCI    C12Q0001-04 [ICM,7]; C12N0001-21 [ICS,7]; C07K0014-335 [ICS,7];
                C07K0014-195 [ICS,7,C*]
        IPCR    C12N0015-09 [I,C*]; C12N0015-09 [I,A]; A61K0039-02 [I,C*];
                A61K0039-02 [I,A]; A61P0031-00 [I,C*]; A61P0031-04 [I,A];
                C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-15 [I,C*];
                C12N0001-15 [I,A]; C12N0001-19 [I,C*]; C12N0001-19 [I,A];
                C12N0001-20 [I,C*]; C12N0001-20 [I,A]; C12N0001-21 [I,C*];
                C12N0001-21 [I,A]; C12N0005-10 [I,C*]; C12N0005-10 [I,A];
                C12N0015-31 [I,C*]; C12N0015-31 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5      ANSWER 14 OF 27  USPATFULL on STN
AN      2005:220997  USPATFULL
TI      Corynebacterium glutamicum genes encoding proteins involved in
        homeostasis and adaptation
IN      Pompejus, Markus, Waldsee, GERMANY, FEDERAL REPUBLIC OF
        Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
        Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
        Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
        Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA      BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF,
        D-67056 (non-U.S. corporation)
PI      US 20050191732     A1  20050901
AI      US 2003-721922     A1  20031124 (10)
RLI     Continuation of Ser. No. US 2000-603124, filed on 23 Jun 2000, ABANDONED
PRAI    DE 1999-19931418    19990708
        DE 1999-19932124    19990709
        DE 1999-19932126    19990709
        DE 1999-19932127    19990709
        DE 1999-19932133    19990709
        DE 1999-19932207    19990709
        DE 1999-19932208    19990709
        DE 1999-19932225    19990709
        DE 1999-19932229    19990709
        DE 1999-19932914    19990709
        DE 1999-19933006    19990709
        DE 1999-19940765    19990827
        DE 1999-19940768    19990827
        DE 1999-19940831    19990827
        DE 1999-19940832    19990827
        DE 1999-19941385    19990831
        DE 1999-19941396    19990831
        DE 1999-19942087    19990903
        US 1999-141031P     19990625 (60)
        US 1999-143694P     19990714 (60)
        US 1999-151778P     19990831 (60)
DT      Utility
FS      APPLICATION
LN.CNT 6552
INCL    INCLM: 435/106.000
        INCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;
                536/023.200
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NCL     NCLM:  435/106.000
        NCLS:  435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;
               536/023.200
IC      [7]
        ICM    C12Q001-68
        ICS    C07H021-04; C12P013-04; C12N009-10; C12N001-21; C12N015-74
        IPCI   C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
               C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C*]; C12N0009-10 [ICS,7];
               C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7]
        IPCR   C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
               C07K0014-34 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
               C12N0009-00 [I,C*]; C12N0009-00 [I,A]; C12N0009-10 [I,C*];
               C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
               C12P0001-04 [I,C*]; C12P0001-04 [I,A]; C12P0013-00 [I,C*];
               C12P0013-04 [I,A]; C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5   ANSWER 15 OF 27  USPATFULL on STN
AN      2005:158196  USPATFULL
TI      Nucleic acid and amino acid sequences relating to streptococcus
        pneumoniae for diagnostics and therapeutics
IN      Doucette-Stamm, Lynn A., Framingham, MA, UNITED STATES
        Bush, David, Somerville, MA, UNITED STATES
PI      US 20050136404     A1  20050623
AI      US 2003-617320     A1  20030710 (10)
RLI     Division of Ser. No. US 1998-107433, filed on 30 Jun 1998, PENDING
PRAI    US 1997-51553P      19970702 (60)
        US 1998-85131P      19980512 (60)
DT      Utility
FS      APPLICATION
LN.CNT 12957
INCL    INCLM: 435/006.000
        INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700
NCL     NCLM:  435/006.000
        NCLS:  435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700
IC      [7]
        ICM    C12Q001-68
        ICS    C07H021-04; C12N001-21; C07K014-315
        IPCI   C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
               C12N0001-21 [ICS,7]; C07K0014-315 [ICS,7]; C07K0014-195
               [ICS,7,C*]
        IPCR   C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
               C07K0014-195 [I,C*]; C07K0014-315 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5   ANSWER 16 OF 27  USPATFULL on STN
AN      2005:131152  USPATFULL
TI      Lactobacillus acidophilus nucleic acid sequences encoding cell surface
        protein homologues and uses therefore
IN      Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
        Alterman, Eric, Apex, NC, UNITED STATES
        Buck, B. Logan, Banner Elk, NC, UNITED STATES
        Russell, W. Michael, Newburg, IN, UNITED STATES
PI      US 20050112612     A1  20050526
        US 7348420         B2  20080325
AI      US 2004-831070     A1  20040423 (10)
PRAI    US 2003-465621P     20030425 (60)
DT      Utility
FS      APPLICATION
LN.CNT 6100
INCL    INCLM: 435/006.000
        INCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 530/350.000;
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                  536/023.200
NCL      NCLM:  536/023.100; 435/006.000
         NCLS:  435/069.100; 435/252.300; 435/320.100; 435/183.000; 530/350.000;
                  536/023.200
IC       [7]
         ICM    C12Q001-68
         ICS    C07H021-04; C12P021-06; C12N009-00; C12N001-21; C07K014-335
         IPCI   C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
                  C12P0021-06 [ICS,7]; C12N0009-00 [ICS,7]; C12N0001-21 [ICS,7];
                  C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
         IPCI-2 C07H0021-04 [I,A]; C07H0021-00 [I,C*]; C12N0001-20 [I,A];
                  C12N0015-00 [I,A]; C12P0001-20 [I,A]
         IPCR   C07H0021-00 [I,C]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
                  C07K0014-335 [I,A]; C12N0001-20 [I,C]; C12N0001-20 [I,A];
                  C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0009-00 [I,C*];
                  C12N0009-00 [I,A]; C12N0015-00 [I,C]; C12N0015-00 [I,A];
                  C12P0021-06 [I,C*]; C12P0021-06 [I,A]; C12Q0001-68 [I,C*];
                  C12Q0001-68 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5    ANSWER 17 OF 27  USPATFULL on STN
AN       2004:95339  USPATFULL
TI       Nutritional formulations containing synbiotic substances
IN       Kaup, Susan M., Collingswood, NJ, UNITED STATES
         Wilson, Jeffrey L., Doylestown, PA, UNITED STATES
         Kostek, Beverley M., Glen Mills, PA, UNITED STATES
         Frantz, David C., Pottstown, PA, UNITED STATES
PA       Wyeth, Madison, NJ, UNITED STATES, 07940 (U.S. corporation)
PI       US 20040072794     A1  20040415
AI       US 2003-681658     A1  20031008 (10)
PRAI     US 2002-418109P       20021011 (60)
DT       Utility
FS       APPLICATION
LN.CNT 542
INCL     INCLM: 514/054.000
         INCLS: 424/093.450
NCL      NCLM:  514/054.000
         NCLS:  424/093.450
IC       [7]
         ICM    A61K045-00
         ICS    A61K031-715
         IPCI   A61K0045-00 [ICM,7]; A61K0031-715 [ICS,7]
         IPCR   A23L0001-052 [I,C*]; A23L0001-0528 [I,A]; A23L0001-29 [I,C*];
                  A23L0001-29 [I,A]; A23L0001-30 [I,C*]; A23L0001-30 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5    ANSWER 18 OF 27  USPATFULL on STN
AN       2004:12970  USPATFULL
TI       Polynucleotides, materials incorporating them, and methods for using
         them
IN       Glenn, Matthew, Whenuapai, NEW ZEALAND
         Havukkala, Ilkka J., Remuera, NEW ZEALAND
         Lubbers, Mark, Palmerston North, NEW ZEALAND
         Dekker, James, Palmerston North, NEW ZEALAND
PA       GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND
         (non-U.S. corporation)
PI       US 20040009490     A1  20040115
         US 7125698         B2  20061024
AI       US 2002-264213     A1  20021003 (10)
RLI      Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,
         PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug
         2000, GRANTED, Pat. No. US 6544772
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PRAI    US 1999-147853P      19990809 (60)
        US 1999-147852P      19990809 (60)
        US 1999-152032P      19990901 (60)
        US 1999-152031P      19990901 (60)
DT      Utility
FS      APPLICATION
LN.CNT 5375
INCL    INCLM: 435/006.000
        INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200
NCL     NCLM:  435/193.000; 435/006.000
        NCLS:  426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;
               435/252.300; 435/320.100; 536/023.200
IC      [7]
        ICM    C12Q001-68
        ICS    C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335
        IPCI   C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
               C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];
               C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
        IPCI-2 C12N0009-10 [I,A]
        IPCR   C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C*];
               A23C0019-032 [I,A]; A61K0038-00 [N,C*]; A61K0038-00 [N,A];
               C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
               C12N0001-21 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5    ANSWER 19 OF 27  USPATFULL on STN
AN      2004:250212  USPATFULL
TI      Nucleic acid and amino acid sequences relating to Streptococcus
        pneumoniae for diagnostics and therapeutics
IN      Doucette-Stamm, Lynn A., Framingham, MA, United States
        Bush, David, Somerville, MA, United States
PA      Genome Therapeutics Corporation, Waltham, MA, United States (U.S.
        corporation)
PI      US 6800744       B1  20041005
AI      US 1998-107433       19980630 (9)
PRAI    US 1998-85131P      19980512 (60)
        US 1997-51553P      19970702 (60)
DT      Utility
FS      GRANTED
LN.CNT 11545
INCL    INCLM: 536/023.100
        INCLS: 435/006.000; 435/320.100; 435/325.000; 435/254.000; 435/419.000;
               536/024.100; 536/023.400; 536/024.320
NCL     NCLM:  536/023.100
        NCLS:  435/006.000; 435/320.100; 435/325.000; 435/419.000; 536/023.400;
               536/024.100; 536/024.320
IC      [7]
        ICM    C12Q001-68
        ICS    C12N001-14; C12N015-00; C12N005-00; C12N005-04; C07H021-02;
               C07H021-04
        IPCI   C12Q0001-68 [ICM,7]; C12N0001-14 [ICS,7]; C12N0015-00 [ICS,7];
               C12N0005-00 [ICS,7]; C12N0005-04 [ICS,7]; C07H0021-02 [ICS,7];
               C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]
        IPCR   C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
               C07K0014-195 [I,C*]; C07K0014-315 [I,A]
EXF     536/23.1; 536/23.4; 536/24.32; 435/320.1; 435/325; 435/254.11; 435/419;
        435/6
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5    ANSWER 20 OF 27  USPATFULL on STN
AN      2003:71519  USPATFULL
TI      Corynebacterium glutamicum genes encoding metabolic pathway proteins
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IN      Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
        Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
        Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
        Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
        Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
        Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF
        Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF
        Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF
PI      US 20030049804     A1   20030313
AI      US 2000-746660     A1   20001222 (9)
RLI     Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
        PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun
        2000, PENDING
PRAI    DE 1999-19931420     19990708
        US 1999-141031P      19990625 (60)
        US 1999-142101P      19990702 (60)
        US 1999-148613P      19990812 (60)
        US 2000-187970P      20000309 (60)
DT      Utility
FS      APPLICATION
LN.CNT 15004
INCL    INCLM: 435/115.000
        INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200
NCL     NCLM:  435/115.000
        NCLS:  435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200
IC      [7]
        ICM    C12P013-08
        ICS    C07H021-04; C12N009-00; C12P021-02; C12N001-21
        IPCI   C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
               C07H0021-00 [ICS,7,C*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];
               C12N0001-21 [ICS,7]
        IPCR   C07K0014-195 [I,C*]; C07K0014-34 [I,A]; C12N0001-21 [I,C*];
               C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
               C12N0009-18 [I,C*]; C12N0009-18 [I,A]; C12N0009-90 [I,C*];
               C12N0009-90 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5   ANSWER 21 OF 27  USPATFULL on STN
AN      2003:95966  USPATFULL
TI      Polynucleotides, materials incorporating them, and methods for using
        them
IN      Glenn, Matthew, Auckland, NEW ZEALAND
        Havukkala, Ilkka J., Auckland, NEW ZEALAND
        Bloksberg, Leonard N., Auckland, NEW ZEALAND
        Lubbers, Mark W., Palmerston North, NEW ZEALAND
        Dekker, James, Palmerston North, NEW ZEALAND
        Christensson, Anna C., Lund, SWEDEN
        Holland, Ross, Palmerson North, NEW ZEALAND
        O'Toole, Paul W., Palmerston North, NEW ZEALAND
        Reid, Julian R., Palmerston North, NEW ZEALAND
        Coolbear, Timothy, Palmerston North, NEW ZEALAND
PA      Genesis Research & Development Corp. Ltd, Parnell, NEW ZEALAND (non-U.S.
        corporation)
        Via Lachia Bioscience (NZ) Ltd., Auckland, NEW ZEALAND (non-U.S.
        corporation)
PI      US 6544772         B1   20030408
AI      US 2000-634238          20000808 (9)
DT      Utility
FS      GRANTED
LN.CNT 2015
INCL    INCLM: 435/252.300
        INCLS: 435/320.100; 536/023.700
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NCL    NCLM:   435/252.300
       NCLS:   435/320.100; 536/023.700
IC     [7]
       ICM     C12N001-21
       ICS     C12N015-63; C12N015-31
       IPCI    C12N0001-21 [ICM,7]; C12N0015-63 [ICS,7]; C12N0015-31 [ICS,7]
       IPCR    A23C0019-00 [I,C*]; A23C0019-032 [I,A]; C07K0014-195 [I,C*];
               C07K0014-335 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
               C12N0015-31 [I,C*]; C12N0015-31 [I,A]
EXF    435/252.3; 435/320.1; 536/23.7
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5     ANSWER 22 OF 27  BIOTECHDS COPYRIGHT 2008 THOMSON REUTERS on STN
AN     1999-00562  BIOTECHDS
TI     Use of lactic and propionic acid bacteria;
           to bind mycotoxin to prevent their absorption or to purify
           contaminated food or feedstuff
AU     El-Nezami H; Kankaanpaa P; Salminen S; Ahokas J
PA     Roy.Melbourne-Inst.Technol.
LO     Melbourne, Victoria, Australia.
PI     WO 9834503 13 Aug 1998
AI     WO 1998-AU63 6 Feb 1998
PRAI   AU 1997-5005 7 Feb 1997
DT     Patent
LA     English
OS     WPI: 1998-557001 [49]


L5     ANSWER 23 OF 27      GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC):              CP000705      GenBank (R)
GenBank ACC. NO. (GBN):   CP000705 AAOV01000000 AAOV01000001-AAOV01000097
GenBank VERSION (VER):    CP000705.1  GI:148530277
SEQUENCE LENGTH (SQL):    1999618
MOLECULE TYPE (CI):       DNA; circular
DIVISION CODE (CI):       Bacteria
DATE (DATE):              17 Oct 2007
DEFINITION (DEF):         Lactobacillus reuteri F275,
                          complete genome.
SOURCE:                   Lactobacillus reuteri F275
 ORGANISM (ORGN):         Lactobacillus reuteri F275
                          Bacteria; Firmicutes; Lactobacillales;
                          Lactobacillaceae; Lactobacillus
PROJECT (PJID):           GenomeProject:15766
COMMENT:
       URL -- http://www.jgi.doe.gov
       JGI Project ID: 4000135
       Source DNA available from Gerald Tannock
       (gerald.tannock@stonebow.otago.ac.nz)
       Bacteria available from DSMZ: DSM 20016
       Contacts: Gerald Tannock (gerald.tannock@stonebow.otago.ac.nz)
                 Paul Richardson (microbes@cuba.jgi-psf.org)
       Quality assurance done by JGI-Stanford
       Annotation done by JGI-ORNL and JGI-PGF
       Finishing done by JGI-PGF
       Finished microbial genomes have been curated to close all gaps with
       greater than 98% coverage of at least two independent clones. Each
       base pair has a minimum q (quality) value of 30 and the total error
       rate is less than one per 50000.
       The JGI and collaborators endorse the principles for the
       distribution and use of large scale sequencing data adopted by the
       larger genome sequencing community and urge users of this data to
       follow them. It is our intention to publish the work of this
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      project in a timely fashion and we welcome collaborative
      interaction on the project and analysis.
      (http://www.genome.gov/page.cfm?pageID=10506376).
REFERENCE:             1  (bases 1 to 1999618)
    AUTHOR (AU):       Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;
                       Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;
                       Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;
                       Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;
                       Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.
    TITLE (TI):        Complete sequence of chromosome of
                       Lactobacillus reuteri DSM 20016
    JOURNAL (SO):      Unpublished
REFERENCE:             2  (bases 1 to 1999618)
    AUTHOR (AU):       Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;
                       Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;
                       Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;
                       Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;
                       Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.
    TITLE (TI):        Direct Submission
    JOURNAL (SO):      Submitted (17-MAY-2007) US DOE Joint Genome Institute,
                       2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698,
                       USA


FEATURES (FEAT):
  Feature Key       Location                 Qualifier
===============+=====================+==================================
source            1..1999618               /organism="Lactobacillus reuteri
                                            F275"
                                            /mol-type="genomic DNA"
                                            /strain="DSM 20016"
                                            /db-xref="taxon:299033"
                                            /note="F275 = DSM 20016 = JCM
                                            1112"



L5   ANSWER 24 OF 27      GENBANK®  COPYRIGHT 2008 on STN

LOCUS (LOC):           AM270397      GenBank (R)
GenBank ACC. NO. (GBN): AM270397
GenBank VERSION (VER): AM270397.1  GI:134084136
CAS REGISTRY NO. (RN): 928607-03-8
SEQUENCE LENGTH (SQL): 163680
MOLECULE TYPE (CI):    DNA; linear
DIVISION CODE (CI):    Plants, fungi, algae
DATE (DATE):           24 Mar 2007
DEFINITION (DEF):      Aspergillus niger contig An18c0040, complete genome.
SOURCE:                Aspergillus niger
 ORGANISM (ORGN):      Aspergillus niger
                       Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                       Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic
                       Trichocomaceae; Aspergillus
REFERENCE:             1  (bases 150631 to 153085)
    AUTHOR (AU):       Habison,A.; Kubicek,C.P.; Rohr,M.
    TITLE (TI):        Partial purification and regulatory properties of
                       phosphofructokinase from Aspergillus niger
    JOURNAL (SO):      Biochem. J., 209 (3), 669-676 (1983)
    OTHER SOURCE (OS): CA 99:171737
REFERENCE:             2  (bases 71863 to 73356)
    AUTHOR (AU):       Manney,T.R.
    TITLE (TI):        Expression of the BAR1 gene in Saccharomyces
                       cerevisiae: induction by the alpha mating pheromone of
                       an activity associated with a secreted protein
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   JOURNAL (SO):        J. Bacteriol., 155 (1), 291-301 (1983)
   OTHER SOURCE (OS):   CA 99:102121
REFERENCE:              3  (bases 71863 to 73356)
   AUTHOR (AU):         Jones,E.W.
   TITLE (TI):          The synthesis and function of proteases in
                        Saccharomyces: genetic approaches
   JOURNAL (SO):        Annu. Rev. Genet., 18, 233-270 (1984)
   OTHER SOURCE (OS):   CA 102:92538
REFERENCE:              4  (bases 144032 to 145578)
   AUTHOR (AU):         Brandsch,R.; Bichler,V.
   TITLE (TI):          In vivo and in vitro expression of the
                        6-hydroxy-D-nicotine oxidase gene of Arthrobacter
                        oxidans, cloned into Escherichia coli, as an
                        enzymatically active, covalently flavinylated
                        polypeptide
   JOURNAL (SO):        FEBS Lett., 192 (2), 204-208 (1985)
   OTHER SOURCE (OS):   CA 104:29597
REFERENCE:              5  (bases 150631 to 153085)
   AUTHOR (AU):         Schreferl,G.; Kubicek,C.P.; Rohr,M.
   TITLE (TI):          Inhibition of citric acid accumulation by manganese
                        ions in Aspergillus niger mutants with reduced citrate
                        control of phosphofructokinase
   JOURNAL (SO):        J. Bacteriol., 165 (3), 1019-1022 (1986)
   OTHER SOURCE (OS):   CA 104:165023
REFERENCE:              6  (bases 156827 to 158638)
   AUTHOR (AU):         Whittington,H.A.; Grant,S.; Roberts,C.F.; Lamb,H.;
                        Hawkins,A.R.
   TITLE (TI):          Identification and isolation of a putative permease
                        gene in the quinic acid utilization (QUT) gene cluster
                        of Aspergillus nidulans
   JOURNAL (SO):        Curr. Genet., 12 (2), 135-139 (1987)
   OTHER SOURCE (OS):   CA 107:91128
REFERENCE:              7  (bases 54105 to 55762)
   AUTHOR (AU):         Chisholm,V.T.; Lea,H.Z.; Rai,R.; Cooper,T.G.
   TITLE (TI):          Regulation of allantoate transport in wild-type and
                        mutant strains of Saccharomyces cerevisiae
   JOURNAL (SO):        J. Bacteriol., 169 (4), 1684-1690 (1987)
   OTHER SOURCE (OS):   CA 106:172689
REFERENCE:              8  (bases 71863 to 73356)
   AUTHOR (AU):         MacKay,V.L.; Welch,S.K.; Insley,M.Y.; Manney,T.R.;
                        Holly,J.; Saari,G.C.; Parker,M.L.
   TITLE (TI):          The Saccharomyces cerevisiae BAR1 gene encodes an
                        exported protein with homology to pepsin
   JOURNAL (SO):        Proc. Natl. Acad. Sci. U.S.A., 85 (1), 55-59 (1988)
   OTHER SOURCE (OS):   CA 108:125658
REFERENCE:              9  (bases 54105 to 55762)
   AUTHOR (AU):         Rai,R.; Genbauffe,F.S.; Cooper,T.G.
   TITLE (TI):          Structure and transcription of the allantoate permease
                        gene (DAL5) from Saccharomyces cerevisiae
   JOURNAL (SO):        J. Bacteriol., 170 (1), 266-271 (1988)
   OTHER SOURCE (OS):   CA 109:17930
REFERENCE:              10
   AUTHOR (AU):         Hawkins,A.R.; Lamb,H.K.; Smith,M.; Keyte,J.W.;
                        Roberts,C.F.
   TITLE (TI):          Molecular organisation of the quinic acid utilization
                        (QUT) gene cluster in Aspergillus nidulans
   JOURNAL (SO):        Mol. Gen. Genet., 214 (2), 224-231 (1988)
   OTHER SOURCE (OS):   CA 111:188522
REFERENCE:              11 (bases 68231 to 69040)
   AUTHOR (AU):         Honjo,M.; Nakayama,A.; Fukazawa,K.; Kawamura,K.;
                        Ando,K.; Furutani,Y.
   TITLE (TI):          A novel Bacillus subtilis gene involved in negative
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                             control of sporulation and degradative-enzyme
                             production
     JOURNAL (SO):           J. Bacteriol., 172 (4), 1783-1790 (1990)
     OTHER SOURCE (OS):      CA 113:146166
REFERENCE:                   12 (bases 5212 to 7379)
     AUTHOR (AU):            Nikawa,J.; Hosaka,K.; Tsukagoshi,Y.; Yamashita,S.
     TITLE (TI):             Primary structure of the yeast choline transport gene
                             and regulation of its expression
     JOURNAL (SO):           J. Biol. Chem., 265 (26), 15996-16003 (1990)
     OTHER SOURCE (OS):      CA 114:18549
REFERENCE:                   13 (bases 159975 to 161849)
     AUTHOR (AU):            Fling,M.E.; Kopf,J.; Tamarkin,A.; Gorman,J.A.;
                             Smith,H.A.; Koltin,Y.
     TITLE (TI):             Analysis of a Candida albicans gene that encodes a
                             novel mechanism for resistance to benomyl and
                             methotrexate
     JOURNAL (SO):           Mol. Gen. Genet., 227 (2), 318-329 (1991)
     OTHER SOURCE (OS):      CA 116:100405
REFERENCE:                   14 (bases 28874 to 30837)
     AUTHOR (AU):            Masuda,N.; Kitamura,N.; Saito,K.
     TITLE (TI):             Primary structure of protein moiety of Penicillium
                             notatum phospholipase B deduced from the cDNA
     JOURNAL (SO):           Eur. J. Biochem., 202 (3), 783-787 (1991)
     OTHER SOURCE (OS):      CA 118:76020
REFERENCE:                   15 (bases 100363 to 101496)
     AUTHOR (AU):            Sakoda,H.; Imanaka,T.
     TITLE (TI):             Cloning and sequencing of the gene coding for alcohol
                             dehydrogenase of Bacillus stearothermophilus and
                             rational shift of the optimum pH
     JOURNAL (SO):           J. Bacteriol., 174 (4), 1397-1402 (1992)
     OTHER SOURCE (OS):      CA 118:186708
REFERENCE:                   16 (bases 20773 to 22555)
     AUTHOR (AU):            Kamoda,S.; Saburi,Y.
     TITLE (TI):             Structural and enzymatical comparison of
                             lignostilbene-alpha,beta-dioxygenase isozymes, I, II,
                             and III, from Pseudomonas paucimobilis TMY1009
     JOURNAL (SO):           Biosci. Biotechnol. Biochem., 57 (6), 931-934 (1993)
     OTHER SOURCE (OS):      CA 119:154577
REFERENCE:                   17 (bases 80602 to 83154)
     AUTHOR (AU):            ElBerry,H.M.; Majumdar,M.L.; Cunningham,T.S.;
                             Sumrada,R.A.; Cooper,T.G.
     TITLE (TI):             Regulation of the urea active transporter gene (DUR3)
                             in Saccharomyces cerevisiae
     JOURNAL (SO):           J. Bacteriol., 175 (15), 4688-4698 (1993)
     OTHER SOURCE (OS):      CA 119:242524
REFERENCE:                   18 (bases 23096 to 24052)
     AUTHOR (AU):            Roper,D.I.; Cooper,R.A.
     TITLE (TI):             Purification, nucleotide sequence and some properties
                             of a bifunctional isomerase/decarboxylase from the
                             homoprotocatechuate degradative pathway of Escherichia
                             coli C
     JOURNAL (SO):           Eur. J. Biochem., 217 (2), 575-580 (1993)
     OTHER SOURCE (OS):      CA 119:265270
REFERENCE:                   19 (bases 5212 to 7379)
     AUTHOR (AU):            Li,Z.; Brendel,M.
     TITLE (TI):             Co-regulation with genes of phospholipid biosynthesis
                             of the CTR/HNM1-encoded choline/nitrogen mustard
                             permease in Saccharomyces cerevisiae
     JOURNAL (SO):           Mol. Gen. Genet., 241 (5-6), 680-684 (1993)
     OTHER SOURCE (OS):      CA 121:28475
REFERENCE:                   20 (bases 159975 to 161849)
     AUTHOR (AU):            Ben-Yaacov,R.; Knoller,S.; Caldwell,G.A.; Becker,J.M.;
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                            Koltin,Y.
   TITLE (TI):             Candida albicans gene encoding resistance to benomyl
                            and methotrexate is a multidrug resistance gene
   JOURNAL (SO):           Antimicrob. Agents Chemother., 38 (4), 648-652 (1994)
   OTHER SOURCE (OS):      CA 121:2236
REFERENCE:                 21 (bases 150631 to 153085)
   AUTHOR (AU):            Legisa,M.; Bencina,M.
   TITLE (TI):             Evidence for the activation of 6-phosphofructo-1-kinase
                            by cAMP-dependent protein kinase in Aspergillus niger
   JOURNAL (SO):           FEMS Microbiol. Lett., 118 (3), 327-333 (1994)
   OTHER SOURCE (OS):      CA 121:102759
REFERENCE:                 22 (bases 138020 to 140061)
   AUTHOR (AU):            Kim,Y.J.; Bjorklund,S.; Li,Y.; Sayre,M.H.;
                            Kornberg,R.D.
   TITLE (TI):             A multiprotein mediator of transcriptional activation
                            and its interaction with the C-terminal repeat domain
                            of RNA polymerase II
   JOURNAL (SO):           Cell, 77 (4), 599-608 (1994)
   OTHER SOURCE (OS):      CA 121:102149
REFERENCE:                 23 (bases 38805 to 39836)
   AUTHOR (AU):            Downs,D.M.; Petersen,L.
   TITLE (TI):             apbA, a new genetic locus involved in thiamine
                            biosynthesis in Salmonella typhimurium
   JOURNAL (SO):           J. Bacteriol., 176 (16), 4858-4864 (1994)
   OTHER SOURCE (OS):      CA 121:197350
REFERENCE:                 24 (bases 5212 to 7379)
   AUTHOR (AU):            Li,Z.; Brendel,M.
   TITLE (TI):             Sensitivity to nitrogen mustard in Saccharomyces
                            cerevisiae is independently determined by regulated
                            choline permease and DNA repair
   JOURNAL (SO):           Mutat. Res., 315 (2), 139-145 (1994)
   OTHER SOURCE (OS):      CA 121:198201
REFERENCE:                 25 (bases 85096 to 90863)
   AUTHOR (AU):            Szczypka,M.S.; Wemmie,J.A.; Moye-Rowley,W.S.;
                            Thiele,D.J.
   TITLE (TI):             A yeast metal resistance protein similar to human
                            cystic fibrosis transmembrane conductance regulator
                            (CFTR) and multidrug resistance-associated protein
   JOURNAL (SO):           J. Biol. Chem., 269 (36), 22853-22857 (1994)
   OTHER SOURCE (OS):      CA 122:26140
REFERENCE:                 26 (bases 91484 to 93088)
   AUTHOR (AU):            Knight,S.A.; Tamai,K.T.; Kosman,D.J.; Thiele,D.J.
   TITLE (TI):             Identification and analysis of a Saccharomyces
                            cerevisiae copper homeostasis gene encoding a
                            homeodomain protein
   JOURNAL (SO):           Mol. Cell. Biol., 14 (12), 7792-7804 (1994)
   OTHER SOURCE (OS):      CA 122:73697
REFERENCE:                 27 (bases 85096 to 90863)
   AUTHOR (AU):            Wemmie,J.A.; Szczypka,M.S.; Thiele,D.J.;
                            Moye-Rowley,W.S.
   TITLE (TI):             Cadmium tolerance mediated by the yeast AP-1 protein
                            requires the presence of an ATP-binding cassette
                            transporter-encoding gene, YCF1
   JOURNAL (SO):           J. Biol. Chem., 269 (51), 32592-32597 (1994)
   OTHER SOURCE (OS):      CA 121:294343
REFERENCE:                 28 (bases 20773 to 22555)
   AUTHOR (AU):            Kamoda,S.; Saburi,Y.
   TITLE (TI):             Cloning of a lignostilbene-alpha,beta-dioxygenase
                            isozyme gene from Pseudomonas paucimobilis TMY1009
   JOURNAL (SO):           Biosci. Biotechnol. Biochem., 59 (10), 1866-1868 (1995)
   OTHER SOURCE (OS):      CA 124:47043
REFERENCE:                 29 (bases 85096 to 90863)
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AUTHOR (AU):            Li,Z.S.; Szczypka,M.; Lu,Y.P.; Thiele,D.J.; Rea,P.A.
TITLE (TI):             The yeast cadmium factor protein (YCF1) is a vacuolar
                        glutathione S-conjugate pump
JOURNAL (SO):           J. Biol. Chem., 271 (11), 6509-6517 (1996)
OTHER SOURCE (OS):      CA 124:226108
REFERENCE:              30 (bases 33419 to 35477)
AUTHOR (AU):            Silva,J.C.; Minto,R.E.; Barry,C.E. III; Holland,K.A.;
                        Townsend,C.A.
TITLE (TI):             Isolation and characterization of the versicolorin B
                        synthase gene from Aspergillus parasiticus. Expansion
                        of the aflatoxin b1 biosynthetic gene cluster
JOURNAL (SO):           J. Biol. Chem., 271 (23), 13600-13608 (1996)
OTHER SOURCE (OS):      CA 125:50401
REFERENCE:              31 (bases 15614 to 17392)
AUTHOR (AU):            Covert,S.F.; Enkerli,J.; Miao,V.P.; VanEtten,H.D.
TITLE (TI):             A gene for maackiain detoxification from a dispensable
                        chromosome of Nectria haematococca
JOURNAL (SO):           Mol. Gen. Genet., 251 (4), 397-406 (1996)
OTHER SOURCE (OS):      CA 125:106677
REFERENCE:              32 (bases 131646 to 132375)
AUTHOR (AU):            Mitsuhashi,S.; Miyachi,S.
TITLE (TI):             Amino acid sequence homology between N- and C-terminal
                        halves of a carbonic anhydrase in Porphyridium
                        purpureum, as deduced from the cloned cDNA
JOURNAL (SO):           J. Biol. Chem., 271 (45), 28703-28709 (1996)
OTHER SOURCE (OS):      CA 125:321312
REFERENCE:              33 (bases 85096 to 90863)
AUTHOR (AU):            Li,Z.S.; Lu,Y.P.; Zhen,R.G.; Szczypka,M.; Thiele,D.J.;
                        Rea,P.A.
TITLE (TI):             A new pathway for vacuolar cadmium sequestration in
                        Saccharomyces cerevisiae: YCF1-catalyzed transport of
                        bis(glutathionato)cadmium
JOURNAL (SO):           Proc. Natl. Acad. Sci. U.S.A., 94 (1), 42-47 (1997)
OTHER SOURCE (OS):      CA 126:127966
REFERENCE:              34 (bases 1241 to 3043)
AUTHOR (AU):            Saito,Y.; Ishii,Y.; Hayashi,H.; Imao,Y.; Akashi,T.;
                        Yoshikawa,K.; Noguchi,Y.; Soeda,S.; Yoshida,M.;
                        Niwa,M.; Hosoda,J.; Shimomura,K.
TITLE (TI):             Cloning of genes coding for L-sorbose and L-sorbosone
                        dehydrogenases from Gluconobacter oxydans and microbial
                        production of 2-keto-L-gulonate, a precursor of
                        L-ascorbic acid, in a recombinant G. oxydans strain
JOURNAL (SO):           Appl. Environ. Microbiol., 63 (2), 454-460 (1997)
OTHER SOURCE (OS):      CA 126:167180
REFERENCE:              35 (bases 150631 to 153085)
AUTHOR (AU):            Ruijter,G.J.; Panneman,H.; Visser,J.
TITLE (TI):             Overexpression of phosphofructokinase and pyruvate
                        kinase in citric acid-producing Aspergillus niger
JOURNAL (SO):           Biochim. Biophys. Acta, 1334 (2-3), 317-326 (1997)
OTHER SOURCE (OS):      CA 126:222695
REFERENCE:              36 (bases 49850 to 51919)
AUTHOR (AU):            Prieto,R.; Woloshuk,C.P.
TITLE (TI):             ord1, an oxidoreductase gene responsible for conversion
                        of O-methylsterigmatocystin to aflatoxin in Aspergillus
                        flavus
JOURNAL (SO):           Appl. Environ. Microbiol., 63 (5), 1661-1666 (1997)
OTHER SOURCE (OS):      CA 127:13942
REFERENCE:              37 (bases 17766 to 20491)
AUTHOR (AU):            Todd,R.B.; Murphy,R.L.; Martin,H.M.; Sharp,J.A.;
                        Davis,M.A.; Katz,M.E.; Hynes,M.J.
TITLE (TI):             The acetate regulatory gene facB of Aspergillus
                        nidulans encodes a Zn(II)2Cys6 transcriptional
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                                activator
   JOURNAL (SO):                Mol. Gen. Genet., 254 (5), 495-504 (1997)
   OTHER SOURCE (OS):           CA 127:105007
REFERENCE:                      38 (bases 71863 to 73356)
   AUTHOR (AU):                 Ballensiefen,W.; Schmitt,H.D.
   TITLE (TI):                  Periplasmic Bar1 protease of Saccharomyces cerevisiae
                                is active before reaching its extracellular destination
   JOURNAL (SO):                Eur. J. Biochem., 247 (1), 142-147 (1997)
   OTHER SOURCE (OS):           CA 127:187926
REFERENCE:                      39 (bases 52148 to 53720)
   AUTHOR (AU):                 Kuroyanagi,N.; Onogi,H.; Wakabayashi,T.; Hagiwara,M.
   TITLE (TI):                  Novel SR-protein-specific kinase, SRPK2, disassembles
                                nuclear speckles
   JOURNAL (SO):                Biochem. Biophys. Res. Commun., 242 (2), 357-364 (1998)
   OTHER SOURCE (OS):           CA 128:241040
REFERENCE:                      40 (bases 113565 to 114733)
   AUTHOR (AU):                 MacDiarmid,C.W.; Gardner,R.C.
   TITLE (TI):                  Overexpression of the Saccharomyces cerevisiae
                                magnesium transport system confers resistance to
                                aluminum ion
   JOURNAL (SO):                J. Biol. Chem., 273 (3), 1727-1732 (1998)
   OTHER SOURCE (OS):           CA 128:177021
REFERENCE:                      41 (bases 135940 to 137166)
   AUTHOR (AU):                 Wang,H.Y.; Lin,W.; Dyck,J.A.; Yeakley,J.M.;
                                Songyang,Z.; Cantley,L.C.; Fu,X.D.
   TITLE (TI):                  SRPK2: a differentially expressed SR protein-specific
                                kinase involved in mediating the interaction and
                                localization of pre-mRNA splicing factors in mammalian
                                cells
   JOURNAL (SO):                J. Cell Biol., 140 (4), 737-750 (1998)
   OTHER SOURCE (OS):           CA 128:306636
REFERENCE:                      42 (bases 38805 to 39836)
   AUTHOR (AU):                 Frodyma,M.E.; Downs,D.
   TITLE (TI):                  ApbA, the ketopantoate reductase enzyme of Salmonella
                                typhimurium is required for the synthesis of thiamine
                                via the alternative pyrimidine biosynthetic pathway
   JOURNAL (SO):                J. Biol. Chem., 273 (10), 5572-5576 (1998)
   OTHER SOURCE (OS):           CA 128:305459
REFERENCE:                      43 (bases 106231 to 106803)
   AUTHOR (AU):                 Woloshuk,C.P.; Prieto,R.
   TITLE (TI):                  Genetic organization and function of the aflatoxin B1
                                biosynthetic genes
   JOURNAL (SO):                FEMS Microbiol. Lett., 160 (2), 169-176 (1998)
   OTHER SOURCE (OS):           CA 128:290649
REFERENCE:                      44 (bases 93571 to 94963)
   AUTHOR (AU):                 Philp,N.J.; Yoon,H.; Grollman,E.F.
   TITLE (TI):                  Monocarboxylate transporter MCT1 is located in the
                                apical membrane and MCT3 in the basal membrane of rat
                                RPE
   JOURNAL (SO):                Am. J. Physiol., 274 (6 PT 2), R1824-R1828 (1998)
   OTHER SOURCE (OS):           CA 129:159493
REFERENCE:                      45 (bases 93571 to 94963)
   AUTHOR (AU):                 Wilson,M.C.; Jackson,V.N.; Heddle,C.; Price,N.T.;
                                Pilegaard,H.; Juel,C.; Bonen,A.; Montgomery,I.;
                                Hutter,O.F.; Halestrap,A.P.
   TITLE (TI):                  Lactic acid efflux from white skeletal muscle is
                                catalyzed by the monocarboxylate transporter isoform
                                MCT3
   JOURNAL (SO):                J. Biol. Chem., 273 (26), 15920-15926 (1998)
   OTHER SOURCE (OS):           CA 129:159801
REFERENCE:                      46 (bases 153410 to 154508)
   AUTHOR (AU):                 Dekkers,L.C.; van der Bij,A.J.; Mulders,I.H.;
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                          Phoelich,C.C.; Wentwoord,R.A.; Glandorf,D.C.;
                          Wijffelman,C.A.; Lugtenberg,B.J.
     TITLE (TI):          Role of the O-antigen of lipopolysaccharide, and
                          possible roles of growth rate and of NADH:ubiquinone
                          oxidoreductase (nuo) in competitive tomato root-tip
                          colonization by Pseudomonas fluorescens WCS365
     JOURNAL (SO):        Mol. Plant Microbe Interact., 11 (8), 763-771 (1998)
     OTHER SOURCE (OS):   CA 129:200426
REFERENCE:                47 (bases 146433 to 148685)
     AUTHOR (AU):         Saito,K.; Yamazaki,H.; Ohnishi,Y.; Fujimoto,S.;
                          Takahashi,E.; Horinouchi,S.
     TITLE (TI):          Production of trehalose synthase from a basidiomycete,
                          Grifola frondosa, in Escherichia coli
     JOURNAL (SO):        Appl. Microbiol. Biotechnol., 50 (2), 193-198 (1998)
     OTHER SOURCE (OS):   CA 130:956
REFERENCE:                48 (bases 122486 to 123895)
     AUTHOR (AU):         Kimura,M.; Matsumoto,G.; Shingu,Y.; Yoneyama,K.;
                          Yamaguchi,I.
     TITLE (TI):          The mystery of the trichothecene 3-O-acetyltransferase
                          gene. Analysis of the region around Tri101 and
                          characterization of its homologue from Fusarium
                          sporotrichioides
     JOURNAL (SO):        FEBS Lett., 435 (2-3), 163-168 (1998)
     OTHER SOURCE (OS):   CA 130:11163
REFERENCE:                49 (bases 146433 to 148685)
     AUTHOR (AU):         Saito,K.; Kase,T.; Takahashi,E.; Horinouchi,S.
     TITLE (TI):          Purification and characterization of a trehalose
                          synthase from the basidiomycete grifola frondosa
     JOURNAL (SO):        Appl. Environ. Microbiol., 64 (11), 4340-4345 (1998)
     OTHER SOURCE (OS):   CA 130:34870
REFERENCE:                50 (bases 14029 to 15172)
     AUTHOR (AU):         Feng,Y.; Khoo,H.E.; Poh,C.L.
     TITLE (TI):          Purification and characterization of gentisate
                          1,2-dioxygenases from Pseudomonas alcaligenes NCIB 9867
                          and Pseudomonas putida NCIB 9869
     JOURNAL (SO):        Appl. Environ. Microbiol., 65 (3), 946-950 (1999)
     OTHER SOURCE (OS):   CA 130:322223
REFERENCE:                51 (bases 59070 to 60560)
     AUTHOR (AU):         Bosch,R.; Moore,E.R.; Garcia-Valdes,E.; Pieper,D.H.
     TITLE (TI):          NahW, a novel, inducible salicylate hydroxylase
                          involved in mineralization of naphthalene by
                          Pseudomonas stutzeri AN10
     JOURNAL (SO):        J. Bacteriol., 181 (8), 2315-2322 (1999)
     OTHER SOURCE (OS):   CA 131:70144
REFERENCE:                52
     AUTHOR (AU):         DeZwaan,T.M.; Carroll,A.M.; Valent,B.; Sweigard,J.A.
     TITLE (TI):          Magnaporthe grisea pth11p is a novel plasma membrane
                          protein that mediates appressorium differentiation in
                          response to inductive substrate cues
     JOURNAL (SO):        Plant Cell, 11 (10), 2013-2030 (1999)
     OTHER SOURCE (OS):   CA 132:47358
REFERENCE:                53 (bases 122486 to 123895)
     AUTHOR (AU):         McCormick,S.P.; Alexander,N.J.; Trapp,S.E.; Hohn,T.M.
     TITLE (TI):          Disruption of TRI101, the gene encoding trichothecene
                          3-O-acetyltransferase, from Fusarium sporotrichioides
     JOURNAL (SO):        Appl. Environ. Microbiol., 65 (12), 5252-5256 (1999)
     OTHER SOURCE (OS):   CA 132:118174
REFERENCE:                54 (bases 111907 to 113460)
     AUTHOR (AU):         Muraguchi,H.; Kamada,T.
     TITLE (TI):          A mutation in the eln2 gene encoding a cytochrome P450
                          of Coprinus cinereus affects mushroom morphogenesis
     JOURNAL (SO):        Fungal Genet. Biol., 29 (1), 49-59 (2000)
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OTHER SOURCE (OS):    CA 134:96073
REFERENCE:            55 (bases 108826 to 111209)
   AUTHOR (AU):       Yu,J.; Chang,P.K.; Bhatnagar,D.; Cleveland,T.E.
   TITLE (TI):        Genes encoding cytochrome P450 and monooxygenase
                      enzymes define one end of the aflatoxin pathway gene
                      cluster in Aspergillus parasiticus
   JOURNAL (SO):      Appl. Microbiol. Biotechnol., 53 (5), 583-590 (2000)
   OTHER SOURCE (OS): CA 133:291807
REFERENCE:            56 (bases 122486 to 123895)
   AUTHOR (AU):       Muhitch,M.J.; McCormick,S.P.; Alexander,N.J.; Hohn,T.M.
   TITLE (TI):        Transgenic expression of the TRI101 or PDR5 gene
                      increases resistance of tobacco to the phytotoxic
                      effects of the trichothecene 4,15-diacetoxyscirpenol
   JOURNAL (SO):      Plant Sci., 157 (2), 201-207 (2000)
   OTHER SOURCE (OS): CA 133:306551
REFERENCE:            57 (bases 107279 to 108340)
   AUTHOR (AU):       Cheng,Q.; Thomas,S.M.; Kostichka,K.; Valentine,J.R.;
                      Nagarajan,V.
   TITLE (TI):        Genetic analysis of a gene cluster for cyclohexanol
                      oxidation in Acinetobacter sp. Strain SE19 by in vitro
                      transposition
   JOURNAL (SO):      J. Bacteriol., 182 (17), 4744-4751 (2000)
   OTHER SOURCE (OS): CA 134:37832
REFERENCE:            58 (bases 100363 to 101496)
   AUTHOR (AU):       Jornvall,H.; Hoog,J.O.; Persson,B.; Pares,X.
   TITLE (TI):        Pharmacogenetics of the alcohol dehydrogenase system
   JOURNAL (SO):      Pharmacology, 61 (3), 184-191 (2000)
   OTHER SOURCE (OS): CA 134:38655
REFERENCE:            59
   AUTHOR (AU):       Calabrese,D.; Bille,J.; Sanglard,D.
   TITLE (TI):        A novel multidrug efflux transporter gene of the major
                      facilitator superfamily from Candida albicans (FLU1)
                      conferring resistance to fluconazole
   JOURNAL (SO):      Microbiology (Reading, Engl.), 146 (PT 11), 2743-2754
                      (2000)
   OTHER SOURCE (OS): CA 135:1055
REFERENCE:            60
   AUTHOR (AU):       Deising,H.B.; Werner,S.; Wernitz,M.
   TITLE (TI):        The role of fungal appressoria in plant infection
   JOURNAL (SO):      Microbes Infect., 2 (13), 1631-1641 (2000)
REFERENCE:            61 (bases 43783 to 45994)
   AUTHOR (AU):       Smith,S.
   TITLE (TI):        The world according to PARP
   JOURNAL (SO):      Trends Biochem. Sci., 26 (3), 174-179 (2001)
   OTHER SOURCE (OS): CA 135:15779
REFERENCE:            62 (bases 131646 to 132375)
   AUTHOR (AU):       Cronk,J.D.; Endrizzi,J.A.; Cronk,M.R.; O'neill,J.W.;
                      Zhang,K.Y.
   TITLE (TI):        Crystal structure of E. coli beta-carbonic anhydrase,
                      an enzyme with an unusual pH-dependent activity
   JOURNAL (SO):      Protein Sci., 10 (5), 911-922 (2001)
REFERENCE:            63 (bases 43783 to 45994)
   AUTHOR (AU):       Ziegler,M.; Oei,S.L.
   TITLE (TI):        A cellular survival switch: poly(ADP-ribosyl)ation
                      stimulates DNA repair and silences transcription
   JOURNAL (SO):      Bioessays, 23 (6), 543-548 (2001)
REFERENCE:            64 (bases 43783 to 45994)
   AUTHOR (AU):       Herceg,Z.; Wang,Z.Q.
   TITLE (TI):        Functions of poly(ADP-ribose) polymerase (PARP) in DNA
                      repair, genomic integrity and cell death
   JOURNAL (SO):      Mutat. Res., 477 (1-2), 97-110 (2001)
   OTHER SOURCE (OS): CA 136:145570
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REFERENCE: 65 (bases 15614 to 17392)
    AUTHOR (AU):   Mundodi,S.R.; Watson,B.S.; Lopez-Meyer,M.; Paiva,N.L.
    TITLE (TI):   Functional expression and subcellular localization of
                         the Nectria haematococca Mak1 phytoalexin
                         detoxification enzyme in transgenic tobacco
    JOURNAL (SO):   Plant Mol. Biol., 46 (4), 421-432 (2001)
    OTHER SOURCE (OS):   CA 135:285870
REFERENCE: 66 (bases 1 to 163680)
    AUTHOR (AU):   Pel,H.J.; de Winde,J.H.; Archer,D.B.; Dyer,P.S.;
                         Hofmann,G.; Schaap,P.J.; Turner,G.; de Vries,R.P.;
                         Albang,R.; Albermann,K.; Andersen,M.R.; Bendtsen,J.D.;
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                         Hombergh,J.P.; van den Hondel,C.A.; van der
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                         Lu,X.; van der Maarel,M.J.; Meulenberg,R.; Menke,H.;
                         Mortimer,M.A.; Nielsen,J.; Oliver,S.G.; Olsthoorn,M.;
                         Pal,K.; van Peij,N.N.; Ram,A.F.; Rinas,U.; Roubos,J.A.;
                         Sagt,C.M.; Schmoll,M.; Sun,J.; Ussery,D.; Varga,J.;
                         Vervecken,W.; van de Vondervoort,P.J.; Wedler,H.;
                         Wosten,H.A.; Zeng,A.P.; van Ooyen,A.J.; Visser,J.;
                         Stam,H.
    TITLE (TI):   Genome sequencing and analysis of the versatile cell
                         factory Aspergillus niger CBS 513.88
    JOURNAL (SO):   Nat. Biotechnol., 25 (2), 221-231 (2007)
    OTHER SOURCE (OS):   CA 146:310276
REFERENCE: 67 (bases 1 to 163680)
    AUTHOR (AU):   Pel,H.J.
    TITLE (TI):   Direct Submission
    JOURNAL (SO):   Submitted (01-MAY-2006) Pel H.J., DSM, 624-0295, P.O.
                         Box 1, 2600 MA Delft, THE NETHERLANDS

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                                              TGAQKPLHGSLCEATSFVGCSSVW
                                              LRGISCSTQYKGKLNIHLNLTSGGRVVTPIPAGF
                                              EHGQGRDLTDELANETLLAFSASP
                                              AASGCRILFFELDLSVLGSSTSVANAAYLQTRCL
                                              V"
    exon   41..325   /locus-tag="An18g00920"
                                              /number=1
    intron   326..416   /locus-tag="An18g00920"
                                              /number=1

exon	417..545	/locus-tag="An18g00920"
		/number=2
gene	874..954	/gene="tRNA-Arg (CCG)"
		/locus-tag="An18e00930"
tRNA	874..954	/gene="tRNA-Arg (CCG)"
		/locus-tag="An18e00930"
		/product="tRNA-Arg"
		/inference="profile:tRNAscan:1.4"
		/note="codon recognized: CGG"
gene	complement(<1241..>3043)	/locus-tag="An18g00940"
mRNA	complement(join(<1241.. 1273,1325..1814, 1867..2175,2229..2599, 2960..>3043))	/locus-tag="An18g00940"
CDS	complement(join(1241..1 273,1325..1814, 1867..2175,2229..2599, 2960..3043))	/locus-tag="An18g00940"
		/EC-number="1.1.99.12"
		/inference="profile:COGS:COG2303"
		/inference="profile:PFAM:PF05199"
		/note="unnamed protein product; Catalytic activity: L-sorbose + acceptor <=> 5-dehydro-D-fructose + reduced acceptor. Cofactor: FAD. Title: strong similarity to FAD dependent L-sorbose dehydrogenase SDH – Gluconobacter oxydans"
		/citation=[34]
		/codon-start=1
		/protein-id="CAK47171.1"
		/db-xref="GI:134084138"
		/translation="MGFVAGFDSDLEWNLRSVPQ ERAFGGDTVSHATNSGKPRNYPLR EKSRRFHEFLGRKQADDMNSGQQLGYSEAFSSSY AGLRSFASSYPLGSNVTLWTKATV ERLIMAGRTAEGVAVARAVGDQIERVQVRARKEV ILSAGAYGSPKILLLSGIGPAAEL KRHNITPVADLPVGKNYADHPHIFTYWTIDECNA TLGDGEMETDQVHWLAGLPYDWMS FAPADTKTQEIAKKILSPTERSRYLADGKMQLEN FIVYTAVDTSARKKPLEGWPGKRV ISLMHVLVDSVSRGTLTLRSSDPADAPVLDPKLL ASPVDRSALYENVRETARAIQAVE GLNAVEFGVDDSLRDNWSNEAIEVRANRSGGSTY HYSGTCAMGEVVDTECRVYQAERL RVVDSGIIPLPLAAHYQAPTYGVAEQAADMILSS VA"
exon	complement(1241..1273)	/locus-tag="An18g00940"
		/number=1
intron	complement(1274..1324)	/locus-tag="An18g00940"
		/number=1
exon	complement(1325..1814)	/locus-tag="An18g00940"
		/number=2
intron	complement(1815..1866)	/locus-tag="An18g00940"
		/number=2
exon	complement(1867..2175)	/locus-tag="An18g00940"
		/number=3
intron	complement(2176..2228)	/locus-tag="An18g00940"
		/number=3
exon	complement(2229..2599)	/locus-tag="An18g00940"

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                                       /number=4
intron          complement(2600..2959) /locus-tag="An18g00940"
                                       /number=4
exon            complement(2960..3043) /locus-tag="An18g00940"
                                       /number=5
gene            complement(<3788..>4775 /locus-tag="An18g00950"
                )
mRNA            complement(join(<3788.. /locus-tag="An18g00950"
                4122,4201..4523,
                4678..>4775))
CDS             complement(join(3788..4 /locus-tag="An18g00950"
                122,4201..4523,
                4678..4775))
                                       /inference="profile:COGS:COG0454"
                                       /inference="profile:COGS:COG0456"
                                       /inference="similar to AA
                                       sequence:UniProtKB:AE010349.4"
                                       /note="unnamed protein product;
                                       Title: weak similarity to
                                       hypothetical acetyltransferase
                                       MK0549 - Methanopyrus kandle"
                                       /codon-start=1
                                       /protein-id="CAK47172.1"
                                       /db-xref="GI:134084139"
                                       /translation="MTKSQFEVREIHTKEEYARL
                                       VDVLWSANFNPYNPVFTAVHPVSG
                                       HTAEDRVKDKALDTEIRWAAHEKNPASHLIYVID
                                       TETGRVAGGCEWLIFHKNPFPNGP
                                       QPLSCTWYPEGSERAEYASRMLSQAFFPRMCWLQ
                                       RPHAGVNAMGVHPDYRRRGVGRLL
                                       MQWGHERIDPLGYESWIEGSPIGRWLYEESGYKR
                                       VISLNIDFAKKNPSDEWNRLVHEC
                                       QPPAILLLWRPPRGEWNDKVPPGPWAVTEDTWK"
exon            complement(3788..4122) /locus-tag="An18g00950"
                                       /number=1
intron          complement(4123..4200) /locus-tag="An18g00950"
                                       /number=1
exon            complement(4201..4523) /locus-tag="An18g00950"
                                       /number=2
intron          complement(4524..4677) /locus-tag="An18g00950"
                                       /number=2
exon            complement(4678..4775) /locus-tag="An18g00950"
                                       /number=3
gene            complement(<5212..>7379 /locus-tag="An18g00960"
                )
mRNA            complement(join(<5212.. /locus-tag="An18g00960"
                5456,5493..5664,
                5746..6075,6140..6159,
                6225..6602,6674..6746,
                6800..6899,
                7249..>7379))
CDS             complement(join(5212..5 /locus-tag="An18g00960"
                456,5493..5664,
                5746..6075,6140..6159,
                6225..6602,6674..6746,
                6800..6899,7249..7379))
                                       /inference="profile:COGS:COG0833"
                                       /inference="similar to AA
                                       sequence:PIR:S11175"
                                       /note="unnamed protein product;
                                       Function: Hnm1 of S. cerevisiae is
                                       the unique coline permease in
```

yeast (Km of 0. 5 micromolar).
Regulation: in S. cerevisiae,
expression of HNM1 gene is
regulated by the phospholipid
precursors inositol and choline
and this regulation involves the
trans-acting factors Ino2p, Ino4p
and Opi1p. Remark: alternate name
for S. cerevisiae Hnm1 is YGL077c.
Similarity: Hnm1 of S. cerevisiae
belongs to the APC family, which
encompasses amino acid permeases
more related to the mammalian
cationic amino-acid transporter
family (Tea/ecoR). Title: strong
similarity to choline permease
Hnm1 -Saccharomyces cerevisiae
plasma membrane"
/citation=[12]
/citation=[19]
/citation=[24]
/codon-start=1
/protein-id="CAK47173.1"
/db-xref="GI:134084140"
/translation="MARNSDVEHSIELRAPTNRD
SGTPSKATFSDDAYELARVGKKEV
GGPAGLVYGFLGVWAGIISVFISMGELASMMPSA
GGQYHWVSILAPRSARKFLSHVTG
SVCIIAWTAAPTAAIYLAASVLQSTIAMNIPSYD
PKGWHITLIMWAILLVCTVLNTWL
GMILPVIEVLILLVHVLGFFAVLVPLVYLGPKAD
PRSIFTVSFDYGGWGDLTLATFIG
LKGTVAAFVGTDGAVHMAEEVANSSRVVPRSMLL
ALMINGATGFAILIAFLFTAGDLL
KIVESSASYPFMYMLASSTGSKGAAVVLSSMMAI
LQACAGLAGISSGSRMLWSFSREQ
AIPGWRWVRQVNQRTLVPFHSTLVVVVAAGLLSL
INIGSAVVLNIILSLVLEAFFASY
MISLTLLLYRGGVLNWGPFRVKGWLGTANNIFAI
AYSIIMMFFGCWPPENHPAPKNIN
YSIVIFAGVTLISIIYYVGWARKHYQGPLAEL"

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intron	complement(5457..5492)	/locus-tag="An18g00960"	/number=1
exon	complement(5493..5664)	/locus-tag="An18g00960"	/number=2
intron	complement(5665..5745)	/locus-tag="An18g00960"	/number=2
exon	complement(5746..6075)	/locus-tag="An18g00960"	/number=3
intron	complement(6076..6139)	/locus-tag="An18g00960"	/number=3
exon	complement(6140..6159)	/locus-tag="An18g00960"	/number=4
intron	complement(6160..6224)	/locus-tag="An18g00960"	/number=4
exon	complement(6225..6602)	/locus-tag="An18g00960"	/number=5
intron	complement(6603..6673)	/locus-tag="An18g00960"	/number=5
exon	complement(6674..6746)	/locus-tag="An18g00960"	

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                                            /number=6
intron          complement(6747..6799)      /locus-tag="An18g00960"
                                            /number=6
exon            complement(6800..6899)      /locus-tag="An18g00960"
                                            /number=7
intron          complement(6900..7248)      /locus-tag="An18g00960"
                                            /number=7
exon            complement(7249..7379)      /locus-tag="An18g00960"
                                            /number=8
gene            complement(<7770..>8415     /locus-tag="An18g00970"
                )
mRNA            complement(join(<7770..     /locus-tag="An18g00970"
                8282,8380..>8415))
CDS             complement(join(7770..8     /locus-tag="An18g00970"
                282,8380..8415))
                                            /note="unnamed protein product;
                                            Title: weak similarity to
                                            hypothetical protein BAA96207.1 -
                                            Oryza sativa"
                                            /codon-start=1
                                            /protein-id="CAK47174.1"
                                            /db-xref="GI:134084141"
                                            /translation="MLCTHAGGEGARSGRPDDRQ
                                            GHQPISVALWLCAPPPGFLSGRTS
                                            LASAGISNPDGATAVNTCETVGCLGLTACGQDCL
                                            SSRAALAELLLGLCCVGDGGGRAF
                                            PANPNKMDRYLLLYCRLGLTLDGPIVVVVVHTLS
                                            LSCSPPTQLHPPPLLASLHSFFPP
                                            ESLGRVPISIYAHMRHAAAKIV"
exon            complement(7770..8282)      /locus-tag="An18g00970"
                                            /number=1
intron          complement(8283..8379)      /locus-tag="An18g00970"
                                            /number=1
exon            complement(8380..8415)      /locus-tag="An18g00970"
                                            /number=2
gene            <8621..>9700                /locus-tag="An18g00980"
mRNA            join(<8621..8764,           /locus-tag="An18g00980"
                8830..9156,9214..9356,
                9406..>9700)
CDS             join(8621..8764,            /locus-tag="An18g00980"
                8830..9156,9214..9356,
                9406..9700)
                                            /note="unnamed protein product;
                                            Function: M. grisea Pth11 is a
                                            pathogenicity gene. Function: M.
                                            grisea Pth11p is likely to be
                                            involved in host surface
                                            recognition. Function: M. grisea
                                            pth11 mutants of strain 4091-5-8
                                            are nonpathogenic due to a defect
                                            in appressorium differentiation.
                                            Localization: in M. grisea, a
                                            Pth11-green fluorescent protein
                                            fusion localised to the cell
                                            membrane and vacuoles. Similarity:
                                            similarity of the predicted A.
                                            niger protein and M. grisea Pth11
                                            is limited to the N-terminal half
                                            of the protein sequences. Title:
                                            weak similarity to integral
                                            membrane protein PTH11 -
                                            Magnaporthe grisea plasma
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                                    membrane"
                                    /citation=[52]
                                    /codon-start=1
                                    /protein-id="CAK47175.1"
                                    /db-xref="GI:134084142"
                                    /translation="MTDHSAAVKVVTCFLLIVSF
                                    IAVVACLTTNWQVLRRKVSSVALL
                                    LSTLIASIASGAAVSVAATHGLGQASPLTDAQVV
                                    VMQKALYSMEVLYVLTLGLGKLSV
                                    MVLFYSLLSSTGQSKSVLAATGLLLIWVVVMVIV
                                    VCLQCHPPEVWNIVGGTCLDLSGI
                                    WIAFGVMNVLVEIMIIAVPSFIIFRLKLSLKRRL
                                    VVISCFGIRILDIAGSIVQLCYVR
                                    NFKIHADSPMPTNVWQWAICSQVLQTVAILSACV
                                    PYLREFLESFPSGMFKPTELKHPT
                                    VQSAYNATKCSDSDIELMRPESTKDT"
sig-peptide      8621..8698         /locus-tag="An18g00980"
                                    /inference="protein
                                    motif:SignalP:2.0"
mat-peptide      join(8699..8764,   /locus-tag="An18g00980"
                 8830..9156,9214..9356,
                 9406..9697)
                                    /product="unnamed"
exon             8621..8764         /locus-tag="An18g00980"
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intron           8765..8829         /locus-tag="An18g00980"
                                    /number=1
exon             8830..9156         /locus-tag="An18g00980"
                                    /number=2
intron           9157..9213         /locus-tag="An18g00980"
                                    /number=2
exon             9214..9356         /locus-tag="An18g00980"
                                    /number=3
intron           9357..9405         /locus-tag="An18g00980"
                                    /number=3
exon             9406..9700         /locus-tag="An18g00980"
                                    /number=4
gene             complement(<9787..>9927 /locus-tag="An18g00990"
                 )
mRNA             complement(<9787..>9927 /locus-tag="An18g00990"
                 )
CDS              complement(9787..9927)  /locus-tag="An18g00990"
                                    /note="unnamed protein product;
                                    Title: strong similarity to EST
                                    an-1359 -Aspergillus niger"
                                    /codon-start=1
                                    /protein-id="CAK47176.1"
                                    /db-xref="GI:134084143"
                                    /translation="MRAATLLLVALSAVALALPT
                                    TNNVERAAADANVRQMDELTVAAI SK"
sig-peptide      complement(9877..9927)  /locus-tag="An18g00990"
                                    /inference="protein
                                    motif:SignalP:2.0"
mat-peptide      complement(9790..9876)  /locus-tag="An18g00990"
                                    /product="unnamed"
exon             complement(9787..9927)  /locus-tag="An18g00990"
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gene             <10500..>11479     /locus-tag="An18g01000"
mRNA             join(<10500..10749, /locus-tag="An18g01000"
                 10812..11041,
                 11105..>11479)
CDS              join(10500..10749,  /locus-tag="An18g01000"
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                    10812..11041,
                    11105..11479)
                                            /note="unnamed protein product;
                                            Similarity: the nucleotide
                                            sequence of the ORF shows strong
                                            similarity to the ESTs an-2192 and
                                            an-2204 of A. niger. Title: strong
                                            similarity to EST an-2192
                                            -Aspergillus niger"
                                            /codon-start=1
                                            /protein-id="CAK47177.1"
                                            /db-xref="GI:134084144"
                                            /translation="MYSYEKVNRDDDSDQGLLAE
                                            DSERVAPQPRVSRFPSWTNALLLL
                                            GLLFSLSLNVGWFVFQKGHNVPIQDLDPDAAMAK
                                            QRSPYTGLAWDTHKPYSHHSEYTS
                                            ENATHADEMWESLSMDPMVIAPTWEWAQSKGLSD
                                            SWAFPWDSNRRIYFIKVFHQLHCL
                                            KLMRHSYHELWSGQESSIPAPHIEHCLDSLRQDL
                                            MCKADDTPMPSLQLLNGGGEGQQM
                                            QCKDFDKLVAWSKAPERNACYKRLTDYKPIVHSI
                                            ERYAFCPEDSEHYPTMSKYFEEHG HYADPFSE"
exon                10500..10749            /locus-tag="An18g01000"
                                            /number=1
intron              10750..10811            /locus-tag="An18g01000"
                                            /number=1
exon                10812..11041            /locus-tag="An18g01000"
                                            /number=2
intron              11042..11104            /locus-tag="An18g01000"
                                            /number=2
exon                11105..11479            /locus-tag="An18g01000"
                                            /number=3
gene                <11980..>13464          /locus-tag="An18g01010"
mRNA                join(<11980..12137,     /locus-tag="An18g01010"
                    12198..>13464)
CDS                 join(11980..12137,      /locus-tag="An18g01010"
                    12198..13464)
                                            /inference="profile:COGS:COG0477"
                                            /note="unnamed protein product;
                                            Function: FLU1 of C. albicans
                                            facilitates resistance to
                                            fluconazole and cycloheximide in
                                            the fluconazole-hypersensitive S.
                                            cerevisiae strain YKKB-13 lacking
                                            the ABC (ATP-binding cassette)
                                            transporter gene PDR5. Function:
                                            FLU1 of C. albicans facilitates
                                            resistance to mycophenolic acid in
                                            C. albicans. Function: FLU1 of C.
                                            albicans is involved in the
                                            resistance to azol derivatives in
                                            C. albicans. Function: MDR1 of C.
                                            albicans facilitates resistance to
                                            the anti-mitotic drug benomyl and
                                            to the dihydrofolate reductase
                                            inhibitor methotrexate.
                                            Similarity: N-terminus of the A.
                                            niger protein is app. 120 aa
                                            shorter than in FLU1 of C.
                                            albicans. Similarity: the
                                            predicted A. niger protein shows
                                            strong similarity to fluconazole
```

resistance protein FLU1of C.
albicans, which is a permease
belonging to the major facilitator
superfamily. Title: strong
similarity to fluconazole
resistance protein FLU1 - Candida
albicans"
/citation=[59]
/codon-start=1
/protein-id="CAK47178.1"
/db-xref="GI:134084145"
/translation="MDEEDGHCKETEVTVQSTSP
VDSADYDPFDPQTRSTTYKWITVV
LVAGLSTMVQLSTIIAAPVSPSILAHFHSDNALY
RTLIVSIWELGEIVAPLLWGPLSE
LYGRQWPLNIANLFFVAFLAGTAASTSIQMLIAF
RFLSGAATAASAIGPGIVSDLFPE
ESRGRAMSIMSLTGALGPVVGPIIGSYLGEKAGW
RWAFWLPTIATGTLSLLILVVYRE
TYSVTLQKRKARQQNPESGSKSPEDTDKTASQVF
FKAILRPLRLLIRSPMLILVTFYL
SVVYGYTYLVMTTIAPLFQDVYGFSEGASGLAFL
GLCLGLILGAFLCSFLLDRYVRTA
RARSGTSKPEQRLPPVLIACFVMSGGLFLFGWTA
QYHVQWIAPIIGTGIIGFGLVSTT
ITLQTYVVDLFGIYAASATSAMLVPRNACAAFLP
LAGPPLFDRLGYNWGGTLLALIVL
VFSLMPLIFINYGERLRGKNLLDD"

exon	11980..12137	/locus-tag="An18g01010" /number=1
intron	12138..12197	/locus-tag="An18g01010" /number=1
exon	12198..13464	/locus-tag="An18g01010" /number=2
gene	complement(<14029..>151 72)	/locus-tag="An18g01020"
mRNA	complement(join(<14029. .14318,14411..14845, 14917..>15172))	/locus-tag="An18g01020"
CDS	complement(join(14029.. 14318,14411..14845, 14917..15172))	/locus-tag="An18g01020"

/EC-number="1.13.11.4"
/inference="profile:COGS:COG3435"
/inference="similar to AA
sequence:UniProtKB:AF173167.3"
/note="unnamed protein product;
Complex: the estimated molecular
mass of the purified gentisate 1,
2-dioxygenase of P. alcaligenes
was 154 kDa, with a subunit mass
of 39 kDa. its structure is
deduced to be a tetramer. Remark:
gentisate 1,2-dioxygenase of P.
alcaligenes exhibits typical
saturation kinetics and has an
apparent Km of 92 microM for
gentisate. this enzyme has broad
substrate specificities towards
alkyl and halogenated gentisate
analogs. Similarity: the predicted
A. niger protein shows strong

similarity to gentisate
1,2-dioxygenase of P. alcaligenes
and conserved hypothetical
proteins from other procaryotic
species. Title: strong similarity
to gentisate 1,2-dioxygenases xlnE
- Pseudomonas alcaligenes"
/citation=[50]
/codon-start=1
/protein-id="CAK47179.1"
/db-xref="GI:134084146"
/translation="MSPSACNTGSNGADSAEQLL
QDLKKSNTLPLWTQMTRLNPPEPN
PTAVPFIWRYDSIRPNLLRAGELVTEKQAERRVL
MLVNPARDAPYTTDTLYAGLQLVM
PNETAPAHRHTAFAMRYIIEGNGGFTAVHGKRIK
MQKGDVILTPTWNYHDHGKDGTGP
MIWLDGLDLPNFRHFPVHFVDHYDQPRYPAEDVD
SATSPIVFPWDKMKAELDKAPGTW
AVRRYLRADGSEGGSAERVDAGTSSLPRQETTSA
VYHVIAGSGCSEIGDKTLVWETGD
TFCVPSWYKYRHIAAEGETVYLYRFDDKPMISAL
GFYRSIDTDLATLVSQ"

exon	complement(14029..14318)	/locus-tag="An18g01020"
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intron	complement(14319..14410)	/locus-tag="An18g01020"
		/number=1
exon	complement(14411..14845)	/locus-tag="An18g01020"
		/number=2
intron	complement(14846..14916)	/locus-tag="An18g01020"
		/number=2
exon	complement(14917..15172)	/locus-tag="An18g01020"
		/number=3
gene	<15614..>17392	/locus-tag="An18g01030"
mRNA	join(<15614..15661, 15723..16281, 16347..16503, 16584..16739, 16803..16942, 17034..>17392)	/locus-tag="An18g01030"
CDS	join(15614..15661, 15723..16281, 16347..16503, 16584..16739, 16803..16942, 17034..17392)	/locus-tag="An18g01030"

/inference="profile:COGS:COG0654"
/inference="profile:PFAM:PF01360"
/note="unnamed protein product;
Function: Mak1 from N.
haematococca specifically
hydroxylates the phytoalexins
medicarpin and
maackiain,converting them to less
fungitoxic derivatives.
Localization: heterologous
expression of the Mak1 cDNA

construct in plants indicated that
Mak1 protein accumulates in the
plant cytoplasm, associated with
endoplasmic reticulum membranes.
Similarity: the predicted A. niger
protein shows strong similarity to
Mak1 from the fungal pathogen N.
haematococca. Mak1 belongs to the
flavin-containing mono-oxygenases.
best matches are with putative
salicylate hydroxylases of several
procaryotic species. Title: strong
similarity to maackiain
detoxification protein 1 MAK1 –
Nectria haematococca endoplasmatic
reticulum"
/citation=[31]
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/protein-id="CAK47180.1"
/db-xref="GI:134084147"
/translation="MASTRMSAQSTIADLRVPDY
PSNCLQFTQQLTASATHTLPQKDA
SVRLNIILAGAGLGGLATAIALAQAGHAVKIYEQ
TPVLGEVGAGIQIPSNSTRILFSL
GLQSYLEPYVTAPESISFRRWQNGKVIGLTKLIP
NFVNNFKAPYYVIHRADFHSALCQ
KALDVGVEIELGAKVVDYDPIVGSITLADGTKHS
ADLIVAADGIKSVARNVVLQGDEM
RFQGPGFAAYRAVVDVGKMRRDPDLSWILEKPAL
NIWIGDSRHVMTYTIGAGKAFNMV
LSHPEMTDPGTWKPETALEDMKAEFQGWDPILSK
IIGMVEKTVKWPLLTGTLLQNWTV
GKLVILGDAAHAMVPYMSQGAAMAVEDGIALSRS
LSHMTSRDQLQKALSIFQEVRKKR
AGHMQEASLLNGKLWHFPDGSLQQARDEAMAPEV
QGIPFSHSPNQWSDPATQMWCYGY
DAEEAIDIAWMESLEARVDCVH"

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intron	15662..15722	/locus-tag="An18g01030" /number=1
exon	15723..16281	/locus-tag="An18g01030" /number=2
intron	16282..16346	/locus-tag="An18g01030" /number=2
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intron	16504..16583	/locus-tag="An18g01030" /number=3
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mRNA	join(<17766..17864,	/locus-tag="An18g01040"

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                                         /inference="similar to AA
                                         sequence:UniProtKB:ENU56097.1"
                                         /note="unnamed protein product;
                                         Phenotype: facB recessive loss of
                                         function mutants in A. nidulans
                                         are deficient in acetate induction
                                         of acetyl-CoA synthase, isocitrate
                                         lyase, malate
                                         synthase,acetamidase, and
                                         NADP-isocitrate dehydrogenase.
                                         Similarity: the predicted A. niger
                                         protein shows similarity to
                                         acetate regulatory DNA binding
                                         protein FacB (facB) from A.
                                         nidulans, which belongs to the
                                         GAL4-type zinc cluster
                                         transcriptional activators. Title:
                                         similarity to acetate regulatory
                                         DNA binding protein facB -
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                                         DAPRKENPLSNQSERFSDFAGTEDTIDAMGAVAF
                                         ADEEDCGFFGPSSNIAFLRHLSCA
                                         VAHSASAQKEITSPPLDRVAYDGGFVSATRPSSP
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                                         SLALIHRYFADTGLLFPYIHPPTFFETYAELKDN
                                         SKRVRRTWLGLLNIILAMAKLTAV
                                         SGTTSAETGISESAIYYHRALSLCKGEILRGTTL
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                                         QLGLHSKGASRAFTPLEQEVRKRT
                                         WFGCVVLDRVRANLFLLNRKTIQQANIRVSTLYK
                                         QIANIIDRIYGQNLGCDSPLSIGE
                                         TVGRVLGIENQLFSWVLGLPESLRQVTVQSMREE
                                         IERSEVGDEGHHKLYPLKFRIILT
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                                         ELVSTTGWQKDLLGAWWYSLYYTFNAALVIIGAM
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mRNA            complement(join(<20773. /locus-tag="An18g01050"
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                22180..22303,
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                                        /inference="similar to AA
                                        sequence:PIR:JC4324"
                                        /note="unnamed protein product;
                                        Catalytic activity:
                                        lignostilbene-alpha,beta-dioxygena
                                        se isozymes (LSD-I, II, and III)
                                        of P. paucimobilis catalyse the
                                        reaction
                                        1,2-bis(4-hydroxy-3-methoxyphenyl)
                                        ethylene + O(2) = 2 vanillin
                                        Cofactor:
                                        lignostilbene-alpha,beta-dioxygena
                                        se isozymes (LSD-I, II, and III)
                                        of P. paucimobilis require iron as
                                        a cofactor. Complex: LSD-I, II,
                                        and III consist of alpha
                                        alpha,alpha beta, and beta beta
                                        subunits, respectively. they show
                                        different specificities for
                                        several substrates that are
```

stilbene and styrene derivatives.
Function: LSD of P. paucimobilis
catalyses the oxidative cleavage
of the interphenyl double bond in
the synthetic substrate and
lignin-derived stilbenes. it is
responsible for the degradation of
a diarylpropane-type structure in
lignin. Similarity: the predicted
A. niger protein shows strong
similarity to subunit lsdB of
lignostilbene-alpha,beta-dioxygena
se isozyme LSD-III of P.
paucimobilis and related
dioxygenases from several plant
species. Title: strong similarity
to subunit lsdB of
lignostilbene-alpha,beta-dioxygena
se isozyme LSD-III -Pseudomonas
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GYEARGDGTPDVCYYTVGPDGKFT
EVVWLVAPVVAMIHDFAVTDNWVIFPIIPQLCDI
ERMKQGGEHWQWSPETPLYLGVIP
RRGAKTADVKWFQYKNSFPGHTANAHEDSSGNLI
IDLGLSEKNVFFWWPDAQGNAPEP
SSIRSQLVRFTINPRAEDLNLTEPRILQADNSEF
YRIDDRYATKPHRHVFFDMMDPSL
GTDFARIAPVLGGGYPLYNSLARFDNVTGETEVY
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                                                      /note="unnamed protein product;
                                                      Catalytic activity:
                                                      5-carboxymethyl-2-hydroxymuconate
                                                      delta-isomerase from E. coli
                                                      catalyses the reaction
                                                      5-carboxymethyl-2-hydroxymuconate
                                                      = 5-carboxy-2-oxohept-3-enedioate.
                                                      Pathway:
                                                      5-carboxymethyl-2-hydroxymuconate
                                                      delta-isomerase from E. coli is
                                                      involved in tyrosine and
                                                      phenylalanine metabolism.
                                                      Similarity: the predicted A. niger
                                                      protein shows strong similarity to
                                                      5-carboxymethyl-2-hydroxymuconate
                                                      delta-isomerase from E. coli and
                                                      many putative
                                                      2-hydroxyhepta-2,4-diene-1,
                                                      7-dioate isomerases from several
                                                      procaryotic and eucaryotic
                                                      organisms. Title: strong
                                                      similarity to
                                                      5-carboxymethyl-2-hydroxymuconate
                                                      delta-isomerase -Escherichia coli
                                                      cytoplasm"
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                                                      PFPFIFFKPNTCVHDHGEPVVIPRIAQNDQADYE
                                                      VIGKDAKDVPVESALDYIAAYTVG
                                                      NDISSRKLQRDPAYAGVVPQWGFSKGFDTFAPLG
                                                      PVLVAASEIPDPSQLQLTTIVDGE
                                                      VRQQESVGDLLFDCRYLISYLSQGTTLQKGSVIM
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intron          23572..23666              /locus-tag="An18g01060"
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                26722..27303,
                27423..>27426)
CDS             join(24984..25058,        /locus-tag="An18g01070"
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                26206..26646,
                26722..27303,
                27423..27426)
                                          /inference="profile:COGS:COG0477"
                                          /note="unnamed protein product;
                                          Function: FLU1 of C. albicans
                                          facilitates resistance to
                                          fluconazole and cycloheximide in
                                          the fluconazole-hypersensitive S.
                                          cerevisiae strain YKKB-13 lacking
                                          the ABC (ATP-binding cassette)
                                          transporter gene PDR5. Function:
                                          FLU1 of C. albicans facilitates
                                          resistance to mycophenolic acid in
                                          C. albicans. Function: FLU1 of C.
                                          albicans is involved in the
                                          resistance to azol derivatives in
                                          C. albicans. Function: MDR1 of C.
                                          albicans facilitates resistance to
                                          the anti-mitotic drug benomyl and
                                          to the dihydrofolate reductase
                                          inhibitor methotrexate.
                                          Similarity: N-terminus of the A.
                                          niger protein is app. 120 aa
                                          shorter than in FLU1 of C.
                                          albicans. Similarity: the
                                          predicted A. niger protein shows
                                          strong similarity to fluconazole
                                          resistance protein FLU1of C.
                                          albicans, which is a permease
                                          belonging to the major facilitator
                                          superfamily. Title: similarity to
                                          fluconazole resistance protein
                                          FLU1 - Candida albicans"
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                                                   NTPPFKGVLRPFHYNKDASFFKAV
                                                   ISPLKLLVHPSVCWGIFTYGISLSPQIIMIFNFS
                                                   ALLEASPYFFCSEYVGLMEIGAIV
                                                   GFLLACYGGGYLSDIVNRMIAQRSSSSSIRPEQR
                                                   LISLIPGMAIGPAGCILLAFACGH
                                                   KLHWAAIAVGFGMVSFGTVYTPNIALTYIVHLHQ
                                                   QDAANCLVSISLVKNLVAFTFLYV
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intron	27304..27422	/locus-tag="An18g01070" /number=7
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gene	complement(<27797..>286 67)	/locus-tag="An18g01080"
mRNA	complement(join(<27797. .28220,28259..28342, 28450..28550, 28602..>28667))	/locus-tag="An18g01080"
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exon              complement(28602..28667 /locus-tag="An18g01080"
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mRNA              join(<28874..29683,     /locus-tag="An18g01090"
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                  29925..30837)
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                                        /inference="profile:PFAM:PF01735"
                                        /note="unnamed protein product;
                                        Catalytic activity:
                                        lysophospholipase catalyses the
                                        reaction 2-lysophosphatidylcholine
                                        + H(2)O = glycerophosphocholine +
                                        a fatty acid anion. Pathway:
                                        lysophospholipase is involved in
                                        phospholipid degradation.
                                        Similarity: the predicted A. niger
                                        protein shows strong similarity to
                                        the protein sequences
                                        lysophospholipase (sequence 5 and
                                        sequence 7) of patents
                                        WO0127251-A/5 and WO0127251-A/7
                                        from A. oryzae (AC# AX112082 and
                                        AC# AX112084) and to other fungal
                                        lysophospholipases. Title: strong
                                        similarity to lysophospholipase
                                        from patent WO0127251-A -
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                                       extracellular/secretion proteins"
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                                       VDYWKPEIDRFFTVTNTSAEAATGKAIFEQIATK
                                       YLAGFEVALSDYLGRGFAYEFIPG
                                       QSGGLNTTFSGIRNLSNFINHQMPMPIIHLASVE
                                       PEDAEYYDLLVPSSNGTIFDLTPF
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                                       KGFDRSSLVIGTSADAFNFWYLES
                                       VSNGTLGQFAKRSTTHESSLTKRLSQPANLNALV
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                                       NLSLSTGNTHKSSTLNLVDGSETGQTIPLWGQIQ
                                       PARNVDFIIAWDDSQDADPYSWNN
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                                       HPQFFGCDANLTTTGDDRAPIVLY
                                       MANAPYSAYTNFSFWQTETSRQQMGEIFVNSFDI
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exon	29925..30837	/locus-tag="An18g01090" /number=3
gene	complement(<30960..>322 18)	/locus-tag="An18g01100"
mRNA	complement(join(<30960. .31045,31081..31220, 31273..31630, 31702..>32218))	/locus-tag="An18g01100"
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                           the function of the protein.
                           Similarity: the predicted A. niger
                           protein shows strong similarity to
                           the protein sequence alcohol
                           dehydrogenase (sequence 19) of
                           patent EP0845532-A/19 from an
                           unclassified organism (AC# A92108)
                           and to other zinc-containing
                           dehydrogenases. Title: strong
                           similarity to alcohol
                           dehydrogenase from patent
                           EP0845532-A - Unclassified
                           organism cytoplasm"
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                           EQITERATKRSWLAADEDGVMADYIVYDESVLCK
                           LPAYLDWVQASMIPCAGVTAWSAL
                           KGMRIGQTVLVQGTGGVSMFALKLALAAGLRVVL
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                           YKNTPEWDEEVLKLTGGVGVDLVVENGGTGSLVK
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                           LSELVPTLIDRRINLRGINAGSKLDMEDFCEALS
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exon            32976..33236             /locus-tag="An18g01110"
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                34080..34956,
                35015..35044,
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CDS             complement(join(33419..  /locus-tag="An18g01120"
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                                        /inference="profile:PFAM:PF05199"
                                        /note="unnamed protein product;
                                        Catalytic activity: versicolorin B
                                        synthase from A. parasiticus
                                        catalyses the side chain
                                        cyclization of racemic versiconal
                                        hemiacetal to the bisfuran ring
                                        system of(-)-versicolorin B.
                                        Pathway: versicolorin B synthase
                                        from A. parasiticus is involved in
                                        the aflatoxin biosynthetic
                                        pathway. Remark: a splice site was
                                        detected upstream of the START
                                        codon. Remark: aflatoxins comprise
                                        a group of polyketide-derived
                                        carcinogenic mycotoxins. Remark:
                                        the genes encoding the aflatoxin
                                        biosynthetic enzymes in A.
                                        parasiticus are clustered. Remark:
                                        versicolorin B synthase from A.
                                        parasiticus possesses an
                                        amino-terminal sequence homologous
                                        to the ADP-binding region of other
                                        flavoenzymes, but does not require
                                        flavin or nicotinamide cofactors
                                        for its cyclase activity.
                                        Similarity: the predicted A. niger
                                        protein shows strong similarity to
                                        versicolorin B synthase from A.
                                        parasiticus and other
                                        oxidoreductases. Title: strong
                                        similarity to versicolorin B
                                        synthase vbs - Aspergillus
                                        parasiticus"
                                        /citation=[30]
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                                        GFVAENVPGANGRSIHYARGKCWGGSSAMNFMIY
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intron	complement(34024..34079)	/locus-tag="An18g01120"
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exon	complement(35095..35477)	/locus-tag="An18g01120"
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CDS	37406..38455	/locus-tag="An18g01130"
		/inference="profile:COGS:COG3000"
		/note="unnamed protein product; Remark: the patent does not provide further information about the function of the protein. Similarity: the predicted A. niger protein shows similarity to the protein fragment (SEQ ID NO:

51484) of patent EP1033405-A2 from
A. thaliana (AC# AAG41385) and to
putative sterol desaturase family
proteins. Title: similarity to
protein fragment SEQ ID NO:51484
from patent EP1033405-A2 -
Arabidopsis thaliana"
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LIAIHQLQVMRRMGHVLGFLDGDQHGRDGVPDVG
VAKVVRSLISTSTFRPIMTVFLSY
RVSQAPAQMSWGWLPLEIGLYGIILDFWFYWYHR
LMHDVGSLWKYHRTHHLTKHPNPL
LTLYADTEQEFFDIAGIPLMTYFSMRLMGMPMGF
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CDS	38805..39836	/locus-tag="An18g01140"

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/inference="profile:PFAM:PF02558"
/note="unnamed protein product;
Title: similarity to ketopantoate
reductase -Salmonella typhimurium
cytoplasm"
/citation=[23]
/citation=[42]
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RHSVICLFQNGLGQIEELNERLFTDPLTRPTYMF
GIMRHGVYIKAPFEAVLAGLTGSC
ALGIVNNDQQASSLSASSTASAQSRFLINRLVEA
PIVRSSELPWMELHQAQLLKLATN
CVVNPLTALLDVRNGSLLANSELQEMRRQLLQEI
SLVFRRLPEFQGLPDVEEQFSVAR
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ILAKSSQGR"

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mRNA	join(<40728..41152,	/locus-tag="An18g01150"

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                      42401..>42671)
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                      42401..42671)

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                                              sequence:UniProtKB:AF188621.1"
                                              /note="unnamed protein product;
                                              Function: FLU1 of C. albicans
                                              facilitates resistance to
                                              fluconazole and cycloheximide in
                                              the fluconazole-hypersensitive S.
                                              cerevisiae strain YKKB-13 lacking
                                              the ABC (ATP-binding cassette)
                                              transporter gene PDR5. Function:
                                              FLU1 of C. albicans facilitates
                                              resistance to mycophenolic acid in
                                              C. albicans. Function: FLU1 of C.
                                              albicans is involved in the
                                              resistance to azol derivatives in
                                              C. albicans. Function: MDR1 of C.
                                              albicans facilitates resistance to
                                              the anti-mitotic drug benomyl and
                                              to the dihydrofolate reductase
                                              inhibitor methotrexate.
                                              Similarity: the predicted A. niger
                                              protein shows strong similarity to
                                              fluconazole resistance protein
                                              FLU1of C. albicans, which is a
                                              permease belonging to the major
                                              facilitator superfamily. Title:
                                              strong similarity to fluconazole
                                              resistance protein FLU1 - Candida
                                              albicans"
                                              /citation=[59]
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                                              SLEYNPQLHTLHSRNTELDLERHRTATSHALSRI
                                              ETQRLQHQLTVGESVKSRASRTPL
                                              PRMGANKDYPPPLPDREDYVVEFDGPEDPLYPQN
                                              WELGTKIYISAILAFTSICSTFDS
                                              AIFSSSTTNVARVFGVGIEVATLSSSLYICGYAS
                                              GPLVWAPLSELKGRKPPIVVAMLG
                                              FGIFNTAVAVAKDLQTIMICRFFCGVFGSCPLAV
                                              VAAVFSDIYNNRTRGVAIAMFSST
                                              VFLGPLLAPFIGGFINTSYLGWRWTAYIPAFMGY
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                                              ELRRRTKNWGIHAKQEEIEVDLRELLVNNFSRPL
                                              RLLFGEPLILAVTIYLSFIYGLLY
                                              CFLTAYTLVFQGVYGMSAGVGGLTLFGMVVGLFI
                                              AASYIIFASRGYNKKLEANGGIPV
                                              PEWRLPPVIIGGALFAGGLFWFGWTGFTKSIHWI
                                              VPTLSGLFTGLGLLIIFIQLFNYL
                                              IDTYLMFAASAIAANTFCRSLVAASFPLFSRQMF
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exon            42401..42671             /locus-tag="An18g01150"
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                                         /locus-tag="An18e01160"
tRNA            42950..43033             /gene="tRNA-His (GTG)"
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                44395..45240,
                45294..45376,
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CDS             join(43783..43852,       /locus-tag="An18g01170"
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                45294..45376,
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                                         /EC-number="2.4.2.30"
                                         /inference="profile:PFAM:PF00644"
                                         /inference="profile:PFAM:PF02877"
                                         /note="unnamed protein product;
                                         Catalytic activity: the NAP
                                         protein of Z. mays catalyses the
                                         reaction NAD(+) +
                                         {ADP-D-ribosyl}(N)-acceptor <=>
                                         nicotinamide +
                                         {ADP-D-ribosyl}(N+1)-acceptor.
                                         Function: the NAP protein of Z.
                                         mays is involved in programmed
                                         cell death or apoptosis.
                                         Localization: the NAP protein of
                                         Z. mays is a nuclear enzyme.
                                         Remark: the ADP-D-ribosyl group of
                                         NAD(+) is transferred to an
                                         acceptor carboxyl group on a
                                         histone or the enzyme itself, and
                                         further ADP-ribosyl groups are
                                         transferred to the 2'-position of
                                         the terminal adenosine moiety,
                                         building up a polymer with an
                                         average chain length of 20-30
                                         units. Remark: the NAP
                                         polynucleotide sequences can be
                                         used for modulation of programmed
                                         cell death in eukaryotic cells.
                                         the method is used, specifically
                                         in plants, to induce, or protect
                                         against, programmed cell
                                         death,depending on the extent to
                                         which PARP activity is reduced.
```

reducing expression of endogenous
NAP class PARP only is also used
to modulate programmed cell death,
to increase growth rate and to
produce plant cells that are more
tolerant of stress (cold, chemical
treatments, pathogens,pests,
drought, heat, etc. , or during
transformation). particular
applications are generation of
plants that are resistant to fungi
or nematodes; are male or female
sterile ; or have better
seed-shatter properties. the
methods are also used to improve
growth of transformed plant cells
(and derived calli or complete
plants). Similarity: the predicted
A. niger protein shows st
rong similarity to the protein
sequence poly(ADP-ribose)
polymerase NAP protein of patent
WO200004173-A1 from Z. mays (AC#
AAY68834) and from many other
eucaryotic organisms. Title:
strong similarity to
poly(ADP-ribose) polymerase NAP
protein from patent WO200004173-A1
- Zea mays nucleus"
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/citation=[63]
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LVESDSAGKKLDEKKFLMGSDIKK
DDEPESPKKRTLEQALGINEDGTTKKLKDAQTVG
TKQINVPVDDTCPLRLTFTVYIDP
TGLIWDATLNQTSATNNNNKFYRIQLLHRNNEFR
TWTHWGRVGEHGQHALLGGGGLDE
AEYEFKKKFKDKSGLTWENRLDPPKKGKYTFIEK
NYEEDTEDEDEDEDKVVAKKPTKP
KAEEVKCTLSAPVQDLVSFIFNKDFFQSTMASMS
YDAQKLPLGKLSKRTLQNGFQALK
DLSELIANPALASTKYDTSFTAAVEHLSNLYFTV
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NMQEMTPLEHTSTEFIELANYLNQ
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GLRIAPPEAPVSGYMFGKGVYFADMSTKSAGYCF
SWGSGNRGLLLLCDVEVGNPMYER
DTASFNAGQEAKAEAKIATLGRGRSIPGGWKDAG
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gene	<46879..>48537	/locus-tag="An18g01180"
mRNA	join(<46879..48454, 48518..>48537)	/locus-tag="An18g01180"
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/EC-number="3.5.1.11"
/note="unnamed protein product;
Function: penicillin V
amidohydrolase (PVA) from F.
oxysporum is used for the
enzymatic hydrolysis of penicillin
V (phenoxy-methylpenicillin) to
6-aminopenicillanic acid (6-APA).
6-APA is the active beta-lactam
nucleus used in the manufacture of
semi-synthetic penicillins.
Similarity: the predicted A. niger
protein shows strong similarity to
the protein sequence penicillin V
amidohydrolase (PVA) of patent
US5516679-A from F. oxysporum (AC#
AAW00291). Title: strong
similarity to penicillin V
amidohydrolase PVA from patent
US5516679-A – Fusarium oxysporum
extracellular/secretion proteins"
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DDTVSVSVWLPLNNWNGRFQATGG
GGLAAGIIGLAPAHPVSQGYATAATDGGLTLNGT
SNPQTGAWILRPDGSINTALLLNF
AHRSIYDMTIIGKTLTERFYGSPPRYSYWSGCST
GGRQGYFAAAKYPNLFDGVLAGAP
ALNFPRLIGYMFWPPVHMFHSAAPPQCVFDTFWK
AIIDECDPLDGATDGLISDYNPQS
CPFKPETLVGHTVTCPEMGSDSPVTITAQHATLV
KQILQGPDLQDHPDLWTGLPPGAS
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NGILGSDDLNLSEFRRAGGKLLTWHGLADELIPA

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tRNA              complement(48889..48960   /gene="tRNA-Ala (AGC)"
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                  51199..51470,
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                                    /note="unnamed protein product;
                                    Function: ord1 of A. flavus
                                    converts O-methylsterigmatocystin
                                    to aflatoxin B1. Pathway: ord1 of
                                    A. flavus catalyzes the last step
                                    of the aflatoxin biosynthetic
                                    pathway. Remark: aflatoxins
                                    comprise a group of
                                    polyketide-derived carcinogenic
                                    mycotoxins. Similarity: the
                                    predicted A. niger protein shows
                                    strong similarity to
                                    O-methylsterigmatocystin
                                    (OMST)-oxidoreductase (ord1) from
                                    A. flavus, which belongs to the
                                    CYP64 family of cytochrome
                                    P450-type monooxygenases. Title:
                                    strong similarity to
                                    O-methylsterigmatocystin
                                    oxidoreductase ord1 - Aspergillus
                                    flavus"
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                52984..53309,
                53368..>53720))
CDS             complement(join(52148.. /locus-tag="An18g01210"
                52359,52411..52573,
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                     52635..52939,
                     52984..53309,
                     53368..53720))
                                        /inference="profile:COGS:COG0515"
                                        /inference="profile:PFAM:PF00069"
                                        /note="unnamed protein product;
                                        Function: SRPK2 from M. musculus
                                        phosphorylates SF2/ASF, a member
                                        of SR splicing factors. Remark:
                                        overexpression of murine SRPK2
                                        causes disassembly of
                                        cotransfected SF2/ASF and
                                        endogenous SC35. SRPK family
                                        members may regulate the
                                        disassembly of the SR proteins in
                                        a tissue-specific manner.
                                        Similarity: the predicted A. niger
                                        protein shows similarity to SRPK2
                                        from M. musculus and strong
                                        similarity to putative
                                        serine/threonine protein kinases
                                        from several eucaryotic organisms.
                                        Title: similarity to
                                        SR-protein-specific kinase SRPK2 -
                                        Mus musculus nucleus"
                                        /citation=[39]
                                        /codon-start=1
                                        /protein-id="CAK47196.1"
                                        /db-xref="GI:134084163"
                                        /translation="MAGRITQCARRLGLLHAKLH
                                        LSCRHSMPTPTPHLRNITRASYQT
                                        IRYSSQWKSSLTVFPTTDALIDPSIEIEEETLPT
                                        YHPEKYYPVQQGEVLDNRYQVLAK
                                        LGYGVTSTVWLGRDLRDSKYVVLKIYVTGQEKNH
                                        ELEIYNRMNAVEVEHPGRDLVRRL
                                        FDHFTVTGPHGPHVCLVHEPMGMSADTLLQKYIP
                                        GNTMTLDEMKTCIRQLLIALDFLH
                                        SAARIVHTGKDLQLKNLLLPVPNTKTLETLEERE
                                        VNDPSPRKILKDRTIYLSTVYNPG
                                        GSGLPLISDFGEARFGDVEKRDDIMPNMYRAPEV
                                        VLKENWNYKVDIWNVAMVAWDIVI
                                        PRHMFDGRNADGIFDDRVHIAEMIALMGPPPASF
                                        RERCRLAYVFWDEQGNWKDLAPIP
                                        DISLESLGADIPGENREGFFRWLRKALQWNAEDR
                                        PTATEFLFDEWLMEGLRRPNNEDA KT"
     exon                complement(52148..52359 /locus-tag="An18g01210"
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                                        /number=1
     intron              complement(52360..52410 /locus-tag="An18g01210"
                         )
                                        /number=1
     exon                complement(52411..52573 /locus-tag="An18g01210"
                         )
                                        /number=2
     intron              complement(52574..52634 /locus-tag="An18g01210"
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                                        /number=2
     exon                complement(52635..52939 /locus-tag="An18g01210"
                         )
                                        /number=3
     intron              complement(52940..52983 /locus-tag="An18g01210"
                         )
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                                               /number=3
exon              complement(52984..53309  /locus-tag="An18g01210"
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                                               /number=4
intron            complement(53310..53367  /locus-tag="An18g01210"
                  )
                                               /number=4
exon              complement(53368..53720  /locus-tag="An18g01210"
                  )
                                               /number=5
gene              complement(<54105..>557  /locus-tag="An18g01220"
                  62)
mRNA              complement(join(<54105.  /locus-tag="An18g01220"
                  .54731,54787..55334,
                  55392..55500,
                  55559..>55762))
CDS               complement(join(54105..  /locus-tag="An18g01220"
                  54731,54787..55334,
                  55392..55500,
                  55559..55762))
                                               /inference="profile:COGS:COG0477"
                                               /inference="similar to AA
                                               sequence:PIR:S64826"
                                               /note="unnamed protein product;
                                               Function: in S. cerevisiae,
                                               mutants (dal5) that lack
                                               allantoate transport have been
                                               isolated. these strains also
                                               exhibit a 60% loss of allantoin
                                               transport capability. Regulation:
                                               in S. cerevisiae Dal5 appears to
                                               be sensitive to nitrogen
                                               catabolite repression, feedback
                                               inhibition, and trans-inhibition.
                                               Regulation: in S. cerevisiae
                                               allantoate uptake is constitutive.
                                               Similarity: the predicted A. niger
                                               protein shows strong similarity to
                                               allantoate permease gene (DAL5)
                                               from S. cerevisiae, which belongs
                                               to the major facilitator
                                               superfamily. Title: strong
                                               similarity to allantoate permease
                                               Dal5 - Saccharomyces cerevisiae"
                                               /citation=[7]
                                               /citation=[9]
                                               /codon-start=1
                                               /protein-id="CAK47197.1"
                                               /db-xref="GI:134084164"
                                               /translation="MEEKLPGAFSQALPVDRTDD
                                               AVEYLQGHAAADSPQIDLRALRRK
                                               IDWHLIPFMFSCYVLQFLDKVMLNYAAVMGMKTE
                                               LHLAGNEYTNTATWFFLAYLIAEA
                                               PNIYCLQKVPAAKWLGVNVALWGVAAAASAGAKN
                                               YATLLTARVFLGIFEATIGPSLML
                                               ISSQYYTKSEQAPRFTLWYNGLGVAQIIGGLVSF
                                               GFQHVHHGATLAGWRIMFLVIGLV
                                               TVLIGVLTLLFIPDTPMKAKWLSEEEKVALLQHV
                                               SVNQTGVWSSAINLKQIWEGVLDI
                                               QLWLLVLITILISVSSGVVTTYSATLIAGFGYSG
                                               PISALLNMPSGIVSIFFTLLVGFG
                                               IRRTSHRWAWNAFCTIPGIIGGGLLSFLPKSNKA
```

```
                                    GVLIGIYLVNAIVATLPILYQWTM
                                    ANCAGHTKRAFSSALIAGSFSVGNIIGPQTFQAR
                                    DAPEYRPAKIAVLATQAAAAVMSV
                                    VLFAYYVWENRRRDRRYGKVEDSMVDEAKWAGLT
                                    DKENTRFRYVY"
exon            complement(54105..54731 /locus-tag="An18g01220"
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                                    /number=1
intron          complement(54732..54786 /locus-tag="An18g01220"
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intron          complement(55335..55391 /locus-tag="An18g01220"
                )
                                    /number=2
exon            complement(55392..55500 /locus-tag="An18g01220"
                )
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intron          complement(55501..55558 /locus-tag="An18g01220"
                )
                                    /number=3
exon            complement(55559..55762 /locus-tag="An18g01220"
                )
                                    /number=4
gene            <56384..>58444          /locus-tag="An18g01230"
mRNA            join(<56384..56645,     /locus-tag="An18g01230"
                56694..56761,
                56818..57009,
                57069..57368,
                57430..57711,
                57897..58158,
                58326..>58444)
CDS             join(56384..56645,      /locus-tag="An18g01230"
                56694..56761,
                56818..57009,
                57069..57368,
                57430..57711,
                57897..58158,
                58326..58444)
                                    /note="unnamed protein product;
                                    Function: M. grisea Pth11 is a
                                    pathogenicity gene. Function: M.
                                    grisea Pth11p likely is involved
                                    in host surface recognition.
                                    Function: M. grisea pth11 mutants
                                    of strain 4091-5-8 are
                                    nonpathogenic due to a defect in
                                    appressorium differentiation.
                                    Localization: in M. grisea, a
                                    Pth11-green fluorescent protein
                                    fusion localised to the cell
                                    membrane and vacuoles. Similarity:
                                    similarity of the predicted A.
                                    niger protein and M. grisea Pth11
                                    is limited to the N-terminal half
                                    of the protein sequences. Title:
                                    similarity to integral membrane
                                    protein PTH11 - Magnaporthe grisea
                                    plasma membrane"
                                    /citation=[52]
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                                             /codon-start=1
                                             /protein-id="CAK47198.1"
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                                             /translation="MGWVHHASPEVEAESQYRLI
                                             LGVCLGLTLLMIITVCLRLAIRFN
                                             ARRLEASDFVMLVTMVGYLRWIDDPTANRCQIFS
                                             IIYSALCVAQSRYGLGLPLSLRPK
                                             ADLPDYTKLNYAGRPFYQLGIAGFKASLCLNYLR
                                             LISGTSKNFYRILIWAVIAVSTLG
                                             HLAGTLVLIFDCQPVERAWNPNISGSCLPAGPTF
                                             YGLAIFTIICDITIIILPIPLLLQ
                                             LNIKTAQKAGVVCLFLLGLFTTICSILRLTQIHR
                                             VAYGDGNSTMLVLWGTIEFNVGNI
                                             VTCVPFLAPLLKGAVRDFRSYSGRKGYDSRSYAL
                                             QTWSKDPRSQLRSTTSAAPQPKRT
                                             PSEELILESGGVDEGGIHMTVELRVSLEKRPTTE
                                             HDGINSAYASQDQIRPGSYWVDVT
                                             DTSQWSRAEQARPTVPDGIFPAIKPSSIQEESCA
                                             SRETLMVVHPDGQPRAATELCPAH
                                             ASWPVGLETGTKASSTTPSPTRFQPNILSAVKAL
                                             LGPALFHLTH"
exon             56384..56645                /locus-tag="An18g01230"
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intron           56646..56693                /locus-tag="An18g01230"
                                             /number=1
exon             56694..56761                /locus-tag="An18g01230"
                                             /number=2
intron           56762..56817                /locus-tag="An18g01230"
                                             /number=2
exon             56818..57009                /locus-tag="An18g01230"
                                             /number=3
intron           57010..57068                /locus-tag="An18g01230"
                                             /number=3
exon             57069..57368                /locus-tag="An18g01230"
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intron           57369..57429                /locus-tag="An18g01230"
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exon             57430..57711                /locus-tag="An18g01230"
                                             /number=5
intron           57712..57896                /locus-tag="An18g01230"
                                             /number=5
exon             57897..58158                /locus-tag="An18g01230"
                                             /number=6
intron           58159..58325                /locus-tag="An18g01230"
                                             /number=6
exon             58326..58444                /locus-tag="An18g01230"
                                             /number=7
gene             <59070..>60560              /locus-tag="An18g01240"
mRNA             join(<59070..59441,         /locus-tag="An18g01240"
                 59521..59806,
                 59879..60178,
                 60237..60312,
                 60374..>60560)
CDS              join(59070..59441,          /locus-tag="An18g01240"
                 59521..59806,
                 59879..60178,
                 60237..60312,
                 60374..60560)

                                             /inference="profile:COGS:COG0654"
                                             /inference="profile:PFAM:PF01360"
                                             /note="unnamed protein product;
                                             Catalytic activity: NahW of P.
```

stutzeri catalyzes the conversion
salicylate + NADH + O(2) <=>
catechol + NAD(+) + H(2)O + CO(2).
Pathway: NahW of P. stutzeri is
involved in the metabolization of
naphtalene and salicylates (lower
naphtalene degradation pathway).
Similarity: the predicted A. niger
protein shows similarity to
salicylate hydroxylase (nahW) of
P. stutzeri,which belongs to the
NADH-dependent monooxygenase
superfamily. Title: similarity to
salicylate hydroxylase nahW
-Pseudomonas stutzeri"
/citation=

<------User Break------>
          sequence:PIR:S45605"

/note="unnamed protein product;
Catalytic activity: alcohol + NAD+
= aldehyde or ketone + NADH.
Pathway: alcohol dehydrogenase
ADH-T from B. stearothermophilus
is involved in glycolysis /
gluconeogenesis; fatty acid
metabolism; bile acid
biosynthesis; tyrosine metabolism;
glycerolipid metabolism. Remark:
the protein sequence of alcohol
dehydrogenase ADH-T from B.
stearothermophilus NCA1503 is
covered by patent JP04218378-A
(AC# AAR26874). Similarity: the
predicted A. niger protein shows
strong similarity to thermostable
alcohol dehydrogenase ADH-T from
B. stearothermophilus NCA1503,
which belongs to the zinc alcohol
dehydrogenase (ADH) family. Title:
strong similarity to thermostable
alcohol dehydrogenase adhT -
Bacillus stearothermophilus"
/citation=[15]
/citation=[58]
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FGFIRRVCGRCDNCISGCDHHCRE
KRAYGQHDFDVGSFSHGTVWDADAVYPIPEGYDS
AHAAPLLCAGASVWACLTNNGIRP
SDRVGVMGIGGLGHLAIKLARALRYNVVALSSSE
KKREEALEFGASEFYRFPNTQTPN
HIKPVKHLLLCGSSDVDYASWVSHLPSKQNAIDH
ANIYRSLLDLVDTNGTIYHISVTL
KPTPIPLVPFGQKGIRIQGCFITSRRNLQELLEF
AARFDIKPTIMTFPLTRNGLEETI
EKLRAGRIRYRAVLEYQAP"
exon   complement(100363..1011 /locus-tag="An18g01430"
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intron	complement(101142..1012 13)	/locus-tag="An18g01430"
		/number=1
exon	complement(101214..1014 96)	/locus-tag="An18g01430"
		/number=2
gene	<101875..>104542	/locus-tag="An18g01440"
mRNA	join(<101875..101958, 102203..102219, 102259..102360, 102392..102399, 102621..103153, 103205..>104542)	/locus-tag="An18g01440"
CDS	join(101875..101958, 102203..102219, 102259..102360, 102392..102399, 102621..103153, 103205..104542)	/locus-tag="An18g01440"
		/inference="profile:COGS:COG3496" /note="unnamed protein product; Similarity: the predicted A. niger protein shows local similarity to the hypothetical protein mll8086 from M. loti. Title: strong similarity to hypothetical protein CAD70872.1 - Neurospora crassa" /codon-start=1 /protein-id="CAK47217.1" /db-xref="GI:134084184" /translation="MTAKCMVIKKAEEDHTEFLG LHHVGSDKNFDNCVTKEVRGPQIL KKFLLRQWIPAQGGREQQPESLILSPVRKNLPSI SVDGILLHAALLTVNLILKLGGWP GLLKFMLRTFAISSVLAPIGLIGFLFLVSFTPRN IKSLSKDKSVIGKPLLFPITLDHT RLSPIKNNFTFNVLFVGIPVGISCRFGRLLSIDA KHTDEEECTERSSLLRLLQTYFSS WFSFDSARYLHRGDDTLSLENKLNKFLREQNENP AKWPYAYMLSVPRFLWWERSVVTW WYLYSESKELDAVIMEINNSFDEKRNVLFKVRRT RIYTESPEKGFEQLLDCKEEHLDE DKRVFSLIPQHGKYAYKATWKKEIFSSPFEKVGE TVSSTFLDPVVPSSWSGNRSLSNT TTFDPSGAPRMIARLWCKVPPIDPGKASSFQIFS ILLIWTVNVTLATPRILFQAIRLH VMNLMRMMEHPDVRPGSEPRRPSKGERKDAPLKM LHSLFDLHANLQSRMLERFFREYL KHIVASYPGDLEVTYIPCKSVFKTTICLRSTQYS AEGQDPRRLRLEVMDPAFYSRIVN SPNAGTAMAKETKPGRSPADALSSPVIASDITQS LQLLDVTVSENRTYDKACSRISSW VLCLRRWLTSSFMDSFVCKALPPRTQEEYVSCLI QLWLEKLTWDFLSPHQIYRVIRAA MLQWAICWILF"
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exon	102203..102219	/locus-tag="An18g01440"
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intron	102220..102258	/locus-tag="An18g01440"
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exon	102259..102360	/locus-tag="An18g01440"
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intron	102361..102391	/locus-tag="An18g01440"
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exon	102392..102399	/locus-tag="An18g01440"
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intron	102400..102620	/locus-tag="An18g01440"
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exon	102621..103153	/locus-tag="An18g01440"
		/number=5
intron	103154..103204	/locus-tag="An18g01440"
		/number=5
exon	103205..104542	/locus-tag="An18g01440"
		/number=6
gene	<106231..>106803	/locus-tag="An18g01450"
mRNA	join(<106231..106565,	/locus-tag="An18g01450"
	106647..>106803)	
CDS	join(106231..106565,	/locus-tag="An18g01450"
	106647..106803)	

/EC-number="1.14.-.-"
/note="unnamed protein product;
Function: ordA of A. parasiticus
is involved in the aflatoxin
biosynthesis and converts
O-methylsterigmatocystin (OMST) to
aflatoxins B1 or G1 and converts
dihydro-O-methylsterigmatocystin
(DHOMST) to aflatoxins B2 or G2.
Remark: aflatoxins comprise a
group of polyketide-derived
carcinogenic mycotoxins. Remark:
it is assumed that the ORF is
N-terminally shorter and has
another start codon 5' to the
predicted one ; the ORF is around
400 amino acids shorter than most
of the homologues cytochrome p450
proteins. Remark: ordA of A.
parasiticus is also called
cytochrome p450 64, cyp64 or omst
oxidoreductase. Similarity: the
ORF shows similarity to several
cytochrome P450 related proteins
from different species. Title:
strong similarity to
O-methylsterigmatocystin
oxidoreductase ordA - Aspergillus
parasiticus"
/citation=[43]
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/protein-id="CAK47218.1"
/db-xref="GI:134084185"
/translation="MTFNPERFLTTESYQAEHDP
HNLAFGFGRRICPGRGFADSTIFL
TVVRSLQAFRIAKISEDGREIEPIVEYLPGVISH
PKPFAISITPRSKEHESFIRSIEI
EHPWEKGDLVSILSVNVLVVVASKLRVFTILTSL
YRLPLIGNCKPPNLLLGRMGLIRF SLH"

exon	106231..106565	/locus-tag="An18g01450"
		/number=1

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                                        /number=1
exon            106647..106803          /locus-tag="An18g01450"
                                        /number=2
gene            <107279..>108340        /locus-tag="An18g01460"
mRNA            join(<107279..107327,   /locus-tag="An18g01460"
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                107795..107907,
                107966..107988,
                108045..108097,
                108151..>108340)
CDS             join(107279..107327,    /locus-tag="An18g01460"
                107380..107740,
                107795..107907,
                107966..107988,
                108045..108097,
                108151..108340)
                                        /EC-number="1.-.-.-"
                                        /inference="profile:COGS:COG1028"
                                        /inference="profile:PFAM:PF00106"
                                        /note="unnamed protein product;
                                        Catalytic activity: cyclohexanol
                                        dehydrogenases convert
                                        cyclohexanol + NAD(+) <=>
                                        cyclohexanone + NADH. Function:
                                        chnA of A. sp. is an alcohol
                                        dehydrogenases proposed to
                                        catalyze the conversion of
                                        cyclohexanol to cyclohexanone (EC
                                        1. 1. 1. 245). Phenotype:
                                        cyclohexanol was detected as the
                                        major intermediate accumulated in
                                        the chnA mutant of A. sp. Remark:
                                        chnA of A. sp. is encoded in the
                                        gene cluster for cyclohexanol
                                        oxidation. Similarity: the ORF
                                        shows similarity to several
                                        dehydrogenases from different
                                        species and with various
                                        specificities. Title: strong
                                        similarity to cyclohexanol
                                        dehydrogenase chnA - Acinetobacter
                                        sp"
                                        /citation=[57]
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                                        /protein-id="CAK47219.1"
                                        /db-xref="GI:134084186"
                                        /translation="MAHLLQGTAFITGAGSGIGA
                                        GVARTFIQNGISKLALVDINLSIL
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                                        KAATTFGRVDIGVNSAGVGDPGEP
                                        TDRLSLKDWQRTVHINQTGVWLSQRALIQQMLTQ
                                        KSRGTRHGRGVIVNVCSSLGITAS
                                        ATGIPFPAYTSSKHGVMGLTKMDAKYYAPSGIRI
                                        NAVCPGFVDTPMVSKAVDSGVFKK
                                        EVESAPVGRIGDVEEITDSILFLASPMSSFIYGA
                                        GLVVDGGYGL"
sig-peptide     join(107279..107327,    /locus-tag="An18g01460"
                107380..107387)
                                        /inference="protein
                                        motif:SignalP:2.0"
mat-peptide     join(107388..107740,    /locus-tag="An18g01460"
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                   107966..107988,
                   108045..108097,
                   108151..108337)
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intron             107328..107379           /locus-tag="An18g01460"
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exon               107380..107740           /locus-tag="An18g01460"
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intron             107741..107794           /locus-tag="An18g01460"
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intron             107908..107965           /locus-tag="An18g01460"
                                            /number=3
exon               107966..107988           /locus-tag="An18g01460"
                                            /number=4
intron             107989..108044           /locus-tag="An18g01460"
                                            /number=4
exon               108045..108097           /locus-tag="An18g01460"
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intron             108098..108150           /locus-tag="An18g01460"
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exon               108151..108340           /locus-tag="An18g01460"
                                            /number=6
gene               <108826..>111209         /locus-tag="An18g01470"
mRNA               join(<108826..108944,    /locus-tag="An18g01470"
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                   109089..109305,
                   109377..109778,
                   109841..109905,
                   110160..110181,
                   110244..110293,
                   110355..110492,
                   110524..110752,
                   110866..110960,
                   111135..>111209)
CDS                join(108826..108944,     /locus-tag="An18g01470"
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                   109089..109305,
                   109377..109778,
                   109841..109905,
                   110160..110181,
                   110244..110293,
                   110355..110492,
                   110524..110752,
                   110866..110960,
                   111135..111209)
                                            /EC-number="1.14.-.-"
                                            /inference="profile:COGS:COG0493"
                                            /note="unnamed protein product;
                                            Remark: aflatoxins are
                                            polyketide-derived secondary
                                            metabolites. Remark: moxY of A.
                                            parasiticus is expressed
                                            concurrently with genes involved
                                            in aflatoxin biosynthesis and it
                                            lies on one end of the cluster of
                                            this genes. Therefore moxY of A.
                                            parasiticus is presumably also
```

involved in aflatoxin
biosynthesis. Similarity: the ORF
shows similarity to monooxigenases
from several species and with
different functions. Title: strong
similarity to monooxygenase moxY
-Aspergillus parasiticus"
/citation=[55]
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TQIELCTVLFAFSNMISASTTDTFTQVIIIGAGM
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FFPKQEEILQYIHGVADEFSVALK
LVGHTEWEGADWQDSEQCWEVRLREIPSGRKFTR
RCRILISAVGGLTNPKHVMLQGIE
RFQGNIVHTALWDQETAVAGKNVIVIGNGASATQ
FIPAIADDAASINQFIRHVRKCAP
EEQYWSLLTPEYSIGCKRRVFDNDGYLKCLHRPN
VDITNDPVVAVEEQSITTQSGKRF
PADLIADVDLDYGRCLRLGSLSRSTMSTGEVVMG
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                                       Function: eln2 of C. cinereus
                                       encodes a novel type of microsomal
                                       cytochrome P450 enzyme, with is
                                       involved in mushroom
                                       morphogenesis. Phenotype: a
                                       dominant mutation of the
                                       elongationless2 (eln2) gene of the
                                       mushroom C. cinereus affects
                                       pattern formation in the
                                       development of fruit body
                                       primordia, causing dumpy primordia
                                       which culminate in mature fruit
                                       bodies with short stipes.
                                       Similarity: the ORF shows
                                       similarity to several cytochrome
                                       p450 related proteins from
                                       different species,which have
                                       different cellular functions.
                                       Title: strong similarity to
                                       cytochrome p450 related protein
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                                        an uptake transporter for
                                        inorganic cations, e. g.
                                        magnesium, which presence seems to
                                        be important for resistance to the
                                        toxic effect of aluminum. Remark:
                                        alr2 of S. cerevisiae is also
                                        called YFL050C. Similarity: the
                                        predicted ORF is 395 amino acids
                                        shorter at the N-terminus and 57
                                        amino acids shorter at its
                                        C-terminal end than alr2 of S.
                                        cerevisiae (nearly the same is
                                        true for alr1 of S. cerevisiae).
                                        Title: strong similarity to ion
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                 21   FILE USPATFULL
                  3   FILE USPAT2
                  0*  FILE WATER
                  2   FILE WPIDS
                  2   FILE WPINDEX
L1                QUE LACTOBACILLUS REUTERI AND TOXIN(P) BIND?
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L4           27 S L3 AND (TABLET OR FOOD OR DIETARY SUPLEMENT OR CONFECTIONERY
L5           27 DUP REM L4 (0 DUPLICATES REMOVED)

=> d l5 1

L5   ANSWER 1 OF 27  USPATFULL on STN
AN     2007:296111  USPATFULL
TI     Lactobacillus acidophillus nucleic acid sequences encoding cell surface
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           protein homologues and uses therefore
IN         Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
           Altermann, Eric, Palmerston North, NEW ZEALAND
           Buck, B. Logan, Banner Elk, NC, UNITED STATES
           Russell, W. Michael, Newburgh, IN, UNITED STATES
PA         North Carolina State University, Raleigh, NC, UNITED STATES (U.S.
           corporation)
PI         US 20070258955      A1  20071108
AI         US 2007-701335      A1  20070201 (11)
RLI        Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING
PRAI       US 2003-465621P     20030425 (60)
DT         Utility
FS         APPLICATION
LN.CNT 5104
INCL    INCLM: 424/093.400
        INCLS: 435/252.100; 435/252.900; 435/320.100; 435/006.000; 435/007.100;
               435/070.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100
NCL     NCLM: 424/093.400
        NCLS: 435/006.000; 435/007.100; 435/070.100; 435/252.100; 435/252.900;
              435/320.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100
IC      IPCI   A61K0035-00 [I,A]; A61K0038-00 [I,A]; A61P0001-00 [I,A];
               C07H0021-02 [I,A]; C07H0021-00 [I,C*]; C07K0016-00 [I,A];
               C07K0004-00 [I,A]; C12N0001-20 [I,A]; C12N0015-00 [I,A];
               C12P0021-04 [I,A]; C12Q0001-68 [I,A]
        IPCR   A61K0035-00 [I,C]; A61K0035-00 [I,A]; A61K0038-00 [I,C];
               A61K0038-00 [I,A]; A61P0001-00 [I,C]; A61P0001-00 [I,A];
               C07H0021-00 [I,C]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
               C07K0004-00 [I,C]; C07K0004-00 [I,A]; C07K0014-195 [I,C*];
               C07K0014-335 [I,A]; C07K0016-00 [I,C]; C07K0016-00 [I,A];
               C12N0001-20 [I,C]; C12N0001-20 [I,A]; C12N0001-21 [I,C*];
               C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
               C12N0015-00 [I,C]; C12N0015-00 [I,A]; C12P0021-04 [I,C];
               C12P0021-04 [I,A]; C12P0021-06 [I,C*]; C12P0021-06 [I,A];
               C12Q0001-68 [I,C]; C12Q0001-68 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 2


L5   ANSWER 2 OF 27   USPATFULL on STN
AN         2007:197155  USPATFULL
TI         Lactobacillus acidophilus nucleic acid sequences encoding cell surface
           protein homologues and uses therefore
IN         Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
           Altermann, Eric, Palmerston North, NEW ZEALAND
           Buck, B. Logan, Banner Elk, NC, UNITED STATES
           Russell, W. Michael, Newburgh, IN, UNITED STATES
PA         North Carolina State University, Raleigh, NC, UNITED STATES, 27695-8210
           (U.S. corporation)
PI         US 20070172495      A1  20070726
AI         US 2007-701319      A1  20070201 (11)
RLI        Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING
PRAI       US 2003-465621P     20030425 (60)
DT         Utility
FS         APPLICATION
LN.CNT 5104
INCL    INCLM: 424/234.100
        INCLS: 514/044.000; 435/006.000; 435/007.320; 435/069.100; 435/252.900;
               435/471.000; 530/350.000; 536/023.700
NCL     NCLM: 424/234.100
        NCLS: 435/006.000; 435/007.320; 435/069.100; 435/252.900; 435/471.000;
              514/044.000; 530/350.000; 536/023.700
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IC      IPCI   A61K0048-00 [I,A]; A61K0039-02 [I,A]; C12Q0001-68 [I,A];
               G01N0033-554 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C*];
               C12P0021-06 [I,A]; C07K0014-335 [I,A]; C07K0014-195 [I,C*]
        IPCR   A61K0048-00 [I,C]; A61K0048-00 [I,A]; A61K0039-02 [I,C];
               A61K0039-02 [I,A]; C07H0021-00 [I,C]; C07H0021-04 [I,A];
               C07K0014-195 [I,C]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
               C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
               C12P0021-06 [I,C]; C12P0021-06 [I,A]; C12Q0001-68 [I,C];
               C12Q0001-68 [I,A]; G01N0033-554 [I,C]; G01N0033-554 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 3


L5    ANSWER 3 OF 27   USPATFULL on STN
AN      2007:140436  USPATFULL
TI      Delivery of trefoil peptides
IN      Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
        Steidler, Lothar, Lokeren, BELGIUM
        Remaut, Erik Rene, Lovendegem, BELGIUM
PI      US 20070122427     A1  20070531
AI      US 2007-654879     A1  20070118 (11)
RLI     Division of Ser. No. US 2002-30390, filed on 16 Apr 2002, PENDING A 371
        of International Ser. No. WO 2000-EP6343, filed on 5 Jul 2000
PRAI    EP 1999-870143       19990705
DT      Utility
FS      APPLICATION
LN.CNT 1335
INCL    INCLM: 424/200.100
        INCLS: 435/252.300; 435/252.900
NCL     NCLM:  424/200.100
        NCLS:  435/252.300; 435/252.900
IC      IPCI   A61K0039-02 [I,A]; C12N0001-21 [I,A]
        IPCR   A61K0039-02 [I,C]; A61K0039-02 [I,A]; C12N0001-21 [I,C];
               C12N0001-21 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 4


L5    ANSWER 4 OF 27   USPATFULL on STN
AN      2007:134502  USPATFULL
TI      Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN      Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
        Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
        Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
        Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
        Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA      BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
        (non-U.S. corporation)
PI      US 20070117183     A1  20070524
AI      US 2006-511140     A1  20060828 (11)
RLI     Division of Ser. No. US 2005-55822, filed on 11 Feb 2005, PENDING
        Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED
PRAI    DE 1999-19932125     19990709
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        DE 1999-19932126    19990709
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        DE 1999-19942095    19990903
        DE 1999-19942129    19990903
        US 1999-141031P     19990625 (60)
        US 1999-142101P     19990702 (60)
        US 1999-148613P     19990812 (60)
        US 2000-187970P     20000309 (60)
DT      Utility
FS      APPLICATION
LN.CNT  8386
INCL    INCLM: 435/069.100
        INCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;
               536/023.200
NCL     NCLM:  435/069.100
        NCLS:  435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;
               536/023.200
IC      IPCI   C07H0021-04 [I,A]; C07H0021-00 [I,C*]; C12P0021-06 [I,A];
               C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
               C12N0009-10 [I,A]; C12N0015-74 [I,A]; C12N0001-21 [I,A]
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               C12N0015-74 [I,C]; C12N0015-74 [I,A]; C12P0013-00 [I,C];
               C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0021-06 [I,C];
               C12P0021-06 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 6


L5    ANSWER 6 OF 27   USPATFULL on STN
AN     2007:130427  USPATFULL
TI     Delivery of trefoil peptides
IN     Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF
       Steidler, Lothar, Lokeren, BELGIUM
       Remaut, Erik Rene, Lonendegem, BELGIUM
PA     Vlaams Interuniversitair Instituut voor Biotechnologie, BELGIUM
       (non-U.S. corporation)
PI     US 7220418        B1   20070522
       WO 2001002570   20010111
AI     US 2000-30390            20000705 (10)
       WO 2000-EP6343          20000705
                               20020416   PCT 371 date
PRAI   EP 1999-870143      19990705
DT     Utility
FS     GRANTED
LN.CNT 1334
INCL   INCLM: 424/200.100
       INCLS: 424/093.450; 424/093.200; 424/234.100; 424/192.100; 514/925.000
NCL    NCLM:  424/200.100
       NCLS:  424/093.200; 424/093.450; 424/192.100; 424/234.100; 514/925.000
IC     IPCI   A01N0063-00 [I,A]; A61K0039-02 [I,A]; A61K0039-00 [I,A]
       IPCR   A01N0063-00 [I,C]; A01N0063-00 [I,A]; C12N0015-09 [I,C*];
               C12N0015-09 [I,A]; A61K0035-66 [I,C*]; A61K0035-74 [I,A];
               A61K0038-00 [I,C*]; A61K0038-00 [I,A]; A61K0039-00 [I,C];
               A61K0039-00 [I,A]; A61K0039-02 [I,C]; A61K0039-02 [I,A];
               A61K0048-00 [I,C*]; A61K0048-00 [I,A]; A61P0001-00 [I,C*];
               A61P0001-04 [I,A]; C07K0014-435 [I,C*]; C07K0014-575 [I,A];
               C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0015-16 [I,C*];
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               C12R0001-01 [N,A]
EXF    424/200.1; 424/192.1; 424/184.1; 424/234.1; 424/244.1; 424/246.1;
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       435/252.9
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 7


L5    ANSWER 7 OF 27   IFIPAT  COPYRIGHT 2008 IFI on STN
AN     11053905  IFIPAT;IFIUDB;IFICDB
TI     METHOD OF IMPROVING IMMUNE FUNCTION IN MAMALS USING LACTOBACILLUS
       REUTERI STRAINS
IN     Kang Ho-Jin (KR); Kwon Ik-boo (KR); Lee Dong-Seog (KR); Mollstam Bo (SE)
PA     Unassigned Or Assigned To Individual (68000)
PI     US 2006002907   A1  20060105
AI     US 2002-531651         20021018
       WO 2002-SE1903         20021018
                              20050415   PCT 371 date
                              20050415   PCT 102(e) date
FI     US 2006002907          20060105
DT     Utility; Patent Application - First Publication
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FS     CHEMICAL
       APPLICATION
ED     Entered STN: 9 Jan 2006
       Last Updated on STN: 9 Jan 2006
CLMN   9
GI      1 Figure(s).
       FIG. 1. Confirmation of inhibitory ability against the binding of vero
       cytotoxin(VT) and Gb3 receptor in a culture supernatant of L. reuteri
       through competitive ELISA. Each reacted as follows, on plates coated with
       Gb3, followed by performing ELISA using mAb against VT.


=> d l5 8

L5     ANSWER 8 OF 27   USPATFULL on STN
AN     2006:274450  USPATFULL
TI     Gene products differentially expressed in cancerous cells
IN     Scott, Elizabeth M., Emeryville, CA, UNITED STATES
       Lamson, George, Emeryville, CA, UNITED STATES
       Kassam, Altaf, Emeryville, CA, UNITED STATES
       Zhang, Guozhong, Emeryville, CA, UNITED STATES
       Sakamoto, Doreen, Emeryville, CA, UNITED STATES
       Garcia, Pablo Dominguez, Emeryville, CA, UNITED STATES
       May, Theresa, Emeryville, CA, UNITED STATES
       Kennedy, Giulia C., Emeryville, CA, UNITED STATES
       Kang, Sanmao, Emeryville, CA, UNITED STATES
       Reinhard, Christoph, Emeryville, CA, UNITED STATES
       Jefferson, Ann Bennett, Emeryville, CA, UNITED STATES
PA     Chiron Corporation (U.S. corporation)
PI     US 20060234246      A1  20061019
AI     US 2004-934842      A1  20040902 (10)
RLI    Continuation-in-part of Ser. No. US 2002-165835, filed on 6 Jun 2002,
       ABANDONED Continuation of Ser. No. US 2000-490818, filed on 25 Jan 2000,
       GRANTED, Pat. No. US 6429302 Continuation-in-part of Ser. No. US
       2001-883152, filed on 15 Jun 2001, ABANDONED Continuation-in-part of
       Ser. No. WO 2003-US15465, filed on 16 May 2003, PENDING
PRAI   US 1999-118302P     19990202 (60)
       US 2000-211835P     20000615 (60)
       US 2003-445222P     20030204 (60)
       US 2002-381533P     20020517 (60)
DT     Utility
FS     APPLICATION
LN.CNT 17024
INCL   INCLM: 435/006.000
       INCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;
              530/388.800; 536/023.500
NCL    NCLM:  435/006.000
       NCLS:  435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;
              530/388.800; 536/023.500
IC     IPCI   C12Q0001-68 [I,A]; G01N0033-574 [I,A]; C07H0021-04 [I,A];
              C07H0021-00 [I,C*]; C12P0021-06 [I,A]; C07K0014-82 [I,A];
              C07K0016-30 [I,A]; C07K0016-18 [I,C*]
       IPCR   C12Q0001-68 [I,C]; C12Q0001-68 [I,A]; C07H0021-00 [I,C];
              C07H0021-04 [I,A]; C07K0014-82 [I,C]; C07K0014-82 [I,A];
              C07K0016-18 [I,C]; C07K0016-30 [I,A]; C12P0021-06 [I,C];
              C12P0021-06 [I,A]; G01N0033-574 [I,C]; G01N0033-574 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 9

L5     ANSWER 9 OF 27   USPATFULL on STN
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AN        2006:98984  USPATFULL
TI        Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN        Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
          Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
          Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
          Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
          Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA        BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
          (non-U.S. corporation)
PI        US 20060084152      A1  20060420
AI        US 2005-239674      A1  20050928 (11)
RLI       Continuation of Ser. No. US 2000-746660, filed on 22 Dec 2000, ABANDONED
          Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
          ABANDONED Continuation-in-part of Ser. No. US 2000-603124, filed on 23
          Jun 2000, ABANDONED
PRAI      DE 1999-19932125      19990709
          DE 1999-19932227      19990709
          DE 1999-19932228      19990709
          DE 1999-19932230      19990709
          DE 1999-19933005      19990714
          DE 1999-19933006      19990714
          DE 1999-19940764      19990827
          DE 1999-19940766      19990827
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          DE 1999-19941396      19990831
          DE 1999-19942087      19990903
          DE 1999-19930476      19990701
          DE 1999-19931419      19990708
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          DE 1999-19942088      19990903
          DE 1999-19942124      19990903
          DE 1999-19932928      19990714
          DE 1999-19931415      19990708
          DE 1999-19931424      19990708
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          DE 1999-19931478      19990708
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          DE 1999-19931573      19990708
          DE 1999-19931592      19990708
          DE 1999-19931632      19990708
          DE 1999-19931634      19990708
          DE 1999-19931636      19990708
          DE 1999-19932130      19990708
          DE 1999-19932186      19990709
          DE 1999-19932922      19990714
          DE 1999-19932926      19990714
          DE 1999-19933004      19990714
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              DE 1999-19940765      19990827
              DE 1999-19941380      19990831
              DE 1999-19941394      19990831
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              DE 1999-19942095      19990903
              DE 1999-19942129      19990903
              DE 1999-19932124      19990709
              DE 1999-19932127      19990709
              DE 1999-19932133      19990709
              DE 1999-19932207      19990709
              DE 1999-19932208      19990709
              DE 1999-19932225      19990709
              DE 1999-19932914      19990709
              DE 1999-19940768      19990827
              DE 1999-19940831      19990827
              DE 1999-19941385      19990831
              US 1999-141031P       19990625 (60)
              US 1999-142101P       19990702 (60)
              US 1999-148613P       19990812 (60)
              US 2000-187970P       20000309 (60)
              US 1999-141031P       19990625 (60)
              US 1999-143694P       19990714 (60)
              US 1999-151778P       19990831 (60)
DT       Utility
FS       APPLICATION
LN.CNT 14822
INCL     INCLM: 435/113.000
         INCLS: 435/115.000; 435/252.300
NCL      NCLM:  435/113.000
         NCLS:  435/115.000; 435/252.300
IC       IPCI   C12P0013-12 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
                C12N0001-20 [I,A]
         IPCR   C12P0013-00 [I,C]; C12P0013-12 [I,A]; C12N0001-20 [I,C];
                C12N0001-20 [I,A]; C12P0013-08 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 9


L5    ANSWER 9 OF 27   USPATFULL on STN
AN       2006:98984   USPATFULL
TI       Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN       Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
         Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
         Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
         Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
         Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA       BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
         (non-U.S. corporation)
PI       US 20060084152      A1   20060420
AI       US 2005-239674      A1   20050928 (11)
RLI      Continuation of Ser. No. US 2000-746660, filed on 22 Dec 2000, ABANDONED
         Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
         ABANDONED Continuation-in-part of Ser. No. US 2000-603124, filed on 23
         Jun 2000, ABANDONED
PRAI     DE 1999-19932125      19990709
         DE 1999-19932227      19990709
         DE 1999-19932228      19990709
         DE 1999-19932230      19990709
         DE 1999-19933005      19990714
         DE 1999-19933006      19990714
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DE 1999-19940764      19990827
DE 1999-19940766      19990827
DE 1999-19940832      19990827
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DE 1999-19941379      19990831
DE 1999-19942077      19990903
DE 1999-19942079      19990903
DE 1999-19931418      19990708
DE 1999-19932126      19990709
DE 1999-19932229      19990709
DE 1999-19941396      19990831
DE 1999-19942087      19990903
DE 1999-19930476      19990701
DE 1999-19931419      19990708
DE 1999-19931420      19990708
DE 1999-19932206      19990709
DE 1999-19942088      19990903
DE 1999-19942124      19990903
DE 1999-19932928      19990714
DE 1999-19931415      19990708
DE 1999-19931424      19990708
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DE 1999-19932186      19990709
DE 1999-19932922      19990714
DE 1999-19932926      19990714
DE 1999-19933004      19990714
DE 1999-19940765      19990827
DE 1999-19941380      19990831
DE 1999-19941394      19990831
DE 1999-19942076      19990903
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DE 1999-19942095      19990903
DE 1999-19942129      19990903
DE 1999-19932124      19990709
DE 1999-19932127      19990709
DE 1999-19932133      19990709
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DE 1999-19932225      19990709
DE 1999-19932914      19990709
DE 1999-19940768      19990827
DE 1999-19940831      19990827
DE 1999-19941385      19990831
US 1999-141031P       19990625 (60)
US 1999-142101P       19990702 (60)
US 1999-148613P       19990812 (60)
US 2000-187970P       20000309 (60)
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            US 1999-141031P       19990625 (60)
            US 1999-143694P       19990714 (60)
            US 1999-151778P       19990831 (60)
DT      Utility
FS      APPLICATION
LN.CNT 14822
INCL    INCLM: 435/113.000
        INCLS: 435/115.000; 435/252.300
NCL     NCLM:  435/113.000
        NCLS:  435/115.000; 435/252.300
IC      IPCI   C12P0013-12 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];
               C12N0001-20 [I,A]
        IPCR   C12P0013-00 [I,C]; C12P0013-12 [I,A]; C12N0001-20 [I,C];
               C12N0001-20 [I,A]; C12P0013-08 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.



=> d l5 10

L5    ANSWER 10 OF 27   USPATFULL on STN
AN      2006:211028  USPATFULL
TI      Nucleic acid sequences relating to Bacteroides fragilis for diagnostics
        and therapeutics
IN      Breton, Gary L., Marlboro, MA, UNITED STATES
PA      Oscient Pharmaceuticals Corporation, Waltham, MA, UNITED STATES (U.S.
        corporation)
PI      US 7090973          B1  20060815
AI      US 2000-540209          20000404 (9)
PRAI    US 1999-128705P     19990409 (60)
DT      Utility
FS      GRANTED
LN.CNT 38850
INCL    INCLM: 435/006.000
        INCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330
NCL     NCLM:  435/006.000
        NCLS:  435/091.200; 536/023.500; 536/024.310; 536/024.330
IC      IPCI   C12Q0001-68 [I,A]; C12P0019-34 [I,A]; C12P0019-00 [I,C*];
               C07H0021-02 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C*]
EXF     435/91.1; 435/91.2; 435/6; 435/320.1; 435/325; 435/352.3; 536/23.1;
        536/24.1; 536/23.7; 536/24.32; 536/24.3; 514/44
CAS INDEXING IS AVAILABLE FOR THIS PATENT.



=> d l5 11-15

L5    ANSWER 11 OF 27   USPATFULL on STN
AN      2006:146715  USPATFULL
TI      Nucleic acid and amino acid sequences relating to Staphylococcus
        epidermidis for diagnostics and therapeutics
IN      Doucette-Stamm, Lynn, Framingham, MA, UNITED STATES
        Bush, David, Somerville, MA, UNITED STATES
PA      Wyeth, Madison, NJ, UNITED STATES (U.S. corporation)
PI      US 7060458          B1  20060613
AI      US 1999-450969          19991129 (9)
RLI     Continuation-in-part of Ser. No. US 1998-134001, filed on 13 Aug 1998,
        Pat. No. US 6380370, issued on 30 Apr 2002
PRAI    US 1997-64964P      19971108 (60)
        US 1997-55779P      19970814 (60)
DT      Utility
FS      GRANTED
LN.CNT 35708
INCL    INCLM: 435/069.100
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        INCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320
NCL     NCLM:  435/069.100
        NCLS:  435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320
IC      IPCI   C07H0021-04 [I,A]; C07H0021-00 [I,C*]
        IPCR   C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C*];
               C12N0001-21 [I,A]; C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]
EXF     435/6; 435/91.2; 435/69.1; 536/22.1; 536/23.1; 536/24.3
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5    ANSWER 12 OF 27  USPATFULL on STN
AN      2005:299042  USPATFULL
TI      Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN      Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
        Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
        Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
        Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
        Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA      BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF
        (non-U.S. corporation)
PI      US 20050260707     A1  20051124
AI      US 2005-55822      A1  20050211 (11)
RLI     Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED
PRAI    DE 1999-19932125    19990709
        DE 1999-19932227    19990709
        DE 1999-19932228    19990709
        DE 1999-19932230    19990709
        DE 1999-19933005    19990714
        DE 1999-19933006    19990714
        DE 1999-19940764    19990827
        DE 1999-19940766    19990827
        DE 1999-19940832    19990827
        DE 1999-19941378    19990831
        DE 1999-19941379    19990831
        DE 1999-19942077    19990903
        DE 1999-19942079    19990903
        DE 1999-19931418    19990708
        DE 1999-19932126    19990709
        DE 1999-19932229    19990709
        DE 1999-19941396    19990831
        DE 1999-19942087    19990903
        DE 1999-19930476    19990701
        DE 1999-19931419    19990708
        DE 1999-19931420    19990708
        DE 1999-19932206    19990709
        DE 1999-19942088    19990903
        DE 1999-19942124    19990903
        DE 1999-19932928    19990714
        DE 1999-19931415    19990708
        DE 1999-19931424    19990708
        DE 1999-19931428    19990708
        DE 1999-19931434    19990708
        DE 1999-19931435    19990708
        DE 1999-19931443    19990708
        DE 1999-19931453    19990708
        DE 1999-19931457    19990708
        DE 1999-19931465    19990708
        DE 1999-19931478    19990708
        DE 1999-19931510    19990708
        DE 1999-109931541   19990708
        DE 1999-19931573    19990708
        DE 1999-19931592    19990708
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            DE 1999-19932130      19990708
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            DE 1999-19932926      19990714
            DE 1999-19933004      19990714
            DE 1999-19940765      19990827
            DE 1999-19941380      19990831
            DE 1999-19941394      19990831
            DE 1999-19942076      19990903
            DE 1999-19942086      19990903
            DE 1999-19942095      19990903
            DE 1999-19942129      19990903
            US 1999-141031P       19990625 (60)
            US 1999-142101P       19990702 (60)
            US 1999-148613P       19990812 (60)
            US 2000-187970P       20000309 (60)
DT      Utility
FS      APPLICATION
LN.CNT 8777
INCL    INCLM: 435/069.100
        INCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200
NCL     NCLM:  435/069.100
        NCLS:  435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200
IC      [7]
        ICM    C12P021-06
        ICS    C12P013-04; C07H021-04; C12N001-20; C12N015-74; C12N009-10
        IPCI   C12P0021-06 [ICM,7]; C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C*];
               C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]; C12N0001-20 [ICS,7];
               C12N0015-74 [ICS,7]; C12N0009-10 [ICS,7]
        IPCR   C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
               C07K0014-34 [I,A]; C12N0001-20 [I,C*]; C12N0001-20 [I,A];
               C12N0009-00 [I,C*]; C12N0009-00 [I,A]; C12N0009-10 [I,C*];
               C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
               C12P0013-00 [I,C*]; C12P0013-04 [I,A]; C12P0021-06 [I,C*];
               C12P0021-06 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5    ANSWER 13 OF 27  USPATFULL on STN
AN      2005:268092  USPATFULL
TI      Modified bacterial surface layer proteins
IN      Pouwels, Pieter Hendrik, Rijswijk, NETHERLANDS
        Smit, Egbert, Sittard, NETHERLANDS
        Tielen, Frans, Prinsenbeek, NETHERLANDS
PI      US 20050233408      A1  20051020
AI      US 2003-500307      A1  20021223 (10)
        WO 2002-EP14749         20021223
                                20041122  PCT 371 date
PRAI    EP 2001-310937      20011228
DT      Utility
FS      APPLICATION
LN.CNT 2664
INCL    INCLM: 435/034.000
        INCLS: 530/395.000; 435/252.300
NCL     NCLM:  435/034.000
        NCLS:  435/252.300; 530/395.000
IC      [7]
        ICM    C12Q001-04
        ICS    C12N001-21; C07K014-335
        IPCI   C12Q0001-04 [ICM,7]; C12N0001-21 [ICS,7]; C07K0014-335 [ICS,7];
               C07K0014-195 [ICS,7,C*]
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       IPCR    C12N0015-09 [I,C*]; C12N0015-09 [I,A]; A61K0039-02 [I,C*];
               A61K0039-02 [I,A]; A61P0031-00 [I,C*]; A61P0031-04 [I,A];
               C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-15 [I,C*];
               C12N0001-15 [I,A]; C12N0001-19 [I,C*]; C12N0001-19 [I,A];
               C12N0001-20 [I,C*]; C12N0001-20 [I,A]; C12N0001-21 [I,C*];
               C12N0001-21 [I,A]; C12N0005-10 [I,C*]; C12N0005-10 [I,A];
               C12N0015-31 [I,C*]; C12N0015-31 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5     ANSWER 14 OF 27   USPATFULL on STN
AN     2005:220997  USPATFULL
TI     Corynebacterium glutamicum genes encoding proteins involved in
       homeostasis and adaptation
IN     Pompejus, Markus, Waldsee, GERMANY, FEDERAL REPUBLIC OF
       Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
       Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
       Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
       Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
PA     BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF,
       D-67056 (non-U.S. corporation)
PI     US 20050191732      A1  20050901
AI     US 2003-721922      A1  20031124 (10)
RLI    Continuation of Ser. No. US 2000-603124, filed on 23 Jun 2000, ABANDONED
PRAI   DE 1999-19931418    19990708
       DE 1999-19932124    19990709
       DE 1999-19932126    19990709
       DE 1999-19932127    19990709
       DE 1999-19932133    19990709
       DE 1999-19932207    19990709
       DE 1999-19932208    19990709
       DE 1999-19932225    19990709
       DE 1999-19932229    19990709
       DE 1999-19932914    19990709
       DE 1999-19933006    19990709
       DE 1999-19940765    19990827
       DE 1999-19940768    19990827
       DE 1999-19940831    19990827
       DE 1999-19940832    19990827
       DE 1999-19941385    19990831
       DE 1999-19941396    19990831
       DE 1999-19942087    19990903
       US 1999-141031P     19990625 (60)
       US 1999-143694P     19990714 (60)
       US 1999-151778P     19990831 (60)
DT     Utility
FS     APPLICATION
LN.CNT 6552
INCL   INCLM: 435/106.000
       INCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;
              536/023.200
NCL    NCLM:  435/106.000
       NCLS:  435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;
              536/023.200
IC     [7]
       ICM    C12Q001-68
       ICS    C07H021-04; C12P013-04; C12N009-10; C12N001-21; C12N015-74
       IPCI   C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
              C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C*]; C12N0009-10 [ICS,7];
              C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7]
       IPCR   C07H0021-00 [I,C*]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
              C07K0014-34 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
              C12N0009-00 [I,C*]; C12N0009-00 [I,A]; C12N0009-10 [I,C*];
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            C12N0009-10 [I,A]; C12N0015-74 [I,C*]; C12N0015-74 [I,A];
            C12P0001-04 [I,C*]; C12P0001-04 [I,A]; C12P0013-00 [I,C*];
            C12P0013-04 [I,A]; C12Q0001-68 [I,C*]; C12Q0001-68 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5     ANSWER 15 OF 27  USPATFULL on STN
AN       2005:158196  USPATFULL
TI       Nucleic acid and amino acid sequences relating to streptococcus
         pneumoniae for diagnostics and therapeutics
IN       Doucette-Stamm, Lynn A., Framingham, MA, UNITED STATES
         Bush, David, Somerville, MA, UNITED STATES
PI       US 20050136404      A1  20050623
AI       US 2003-617320      A1  20030710 (10)
RLI      Division of Ser. No. US 1998-107433, filed on 30 Jun 1998, PENDING
PRAI     US 1997-51553P      19970702 (60)
         US 1998-85131P      19980512 (60)
DT       Utility
FS       APPLICATION
LN.CNT 12957
INCL     INCLM: 435/006.000
         INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700
NCL      NCLM:  435/006.000
         NCLS:  435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700
IC       [7]
         ICM    C12Q001-68
         ICS    C07H021-04; C12N001-21; C07K014-315
         IPCI   C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
                C12N0001-21 [ICS,7]; C07K0014-315 [ICS,7]; C07K0014-195
                [ICS,7,C*]
         IPCR   C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
                C07K0014-195 [I,C*]; C07K0014-315 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.



=> d l5 16-20


L5     ANSWER 16 OF 27  USPATFULL on STN
AN       2005:131152  USPATFULL
TI       Lactobacillus acidophilus nucleic acid sequences encoding cell surface
         protein homologues and uses therefore
IN       Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
         Alterman, Eric, Apex, NC, UNITED STATES
         Buck, B. Logan, Banner Elk, NC, UNITED STATES
         Russell, W. Michael, Newburg, IN, UNITED STATES
PI       US 20050112612      A1  20050526
         US 7348420          B2  20080325
AI       US 2004-831070      A1  20040423 (10)
PRAI     US 2003-465621P     20030425 (60)
DT       Utility
FS       APPLICATION
LN.CNT 6100
INCL     INCLM: 435/006.000
         INCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 530/350.000;
                536/023.200
NCL      NCLM:  536/023.100; 435/006.000
         NCLS:  435/069.100; 435/252.300; 435/320.100; 435/183.000; 530/350.000;
                536/023.200
IC       [7]
         ICM    C12Q001-68
         ICS    C07H021-04; C12P021-06; C12N009-00; C12N001-21; C07K014-335
         IPCI   C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
                C12P0021-06 [ICS,7]; C12N0009-00 [ICS,7]; C12N0001-21 [ICS,7];
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                    C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
          IPCI-2 C07H0021-04 [I,A]; C07H0021-00 [I,C*]; C12N0001-20 [I,A];
                 C12N0015-00 [I,A]; C12P0001-20 [I,A]
          IPCR   C07H0021-00 [I,C]; C07H0021-04 [I,A]; C07K0014-195 [I,C*];
                 C07K0014-335 [I,A]; C12N0001-20 [I,C]; C12N0001-20 [I,A];
                 C12N0001-21 [I,C*]; C12N0001-21 [I,A]; C12N0009-00 [I,C*];
                 C12N0009-00 [I,A]; C12N0015-00 [I,C]; C12N0015-00 [I,A];
                 C12P0021-06 [I,C*]; C12P0021-06 [I,A]; C12Q0001-68 [I,C*];
                 C12Q0001-68 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5    ANSWER 17 OF 27   USPATFULL on STN
AN       2004:95339   USPATFULL
TI       Nutritional formulations containing synbiotic substances
IN       Kaup, Susan M., Collingswood, NJ, UNITED STATES
         Wilson, Jeffrey L., Doylestown, PA, UNITED STATES
         Kostek, Beverley M., Glen Mills, PA, UNITED STATES
         Frantz, David C., Pottstown, PA, UNITED STATES
PA       Wyeth, Madison, NJ, UNITED STATES, 07940 (U.S. corporation)
PI       US 20040072794      A1   20040415
AI       US 2003-681658      A1   20031008 (10)
PRAI     US 2002-418109P       20021011 (60)
DT       Utility
FS       APPLICATION
LN.CNT 542
INCL     INCLM: 514/054.000
         INCLS: 424/093.450
NCL      NCLM:  514/054.000
         NCLS:  424/093.450
IC       [7]
         ICM    A61K045-00
         ICS    A61K031-715
         IPCI   A61K0045-00 [ICM,7]; A61K0031-715 [ICS,7]
         IPCR   A23L0001-052 [I,C*]; A23L0001-0528 [I,A]; A23L0001-29 [I,C*];
                A23L0001-29 [I,A]; A23L0001-30 [I,C*]; A23L0001-30 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5    ANSWER 18 OF 27   USPATFULL on STN
AN       2004:12970   USPATFULL
TI       Polynucleotides, materials incorporating them, and methods for using
         them
IN       Glenn, Matthew, Whenuapai, NEW ZEALAND
         Havukkala, Ilkka J., Remuera, NEW ZEALAND
         Lubbers, Mark, Palmerston North, NEW ZEALAND
         Dekker, James, Palmerston North, NEW ZEALAND
PA       GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND
         (non-U.S. corporation)
PI       US 20040009490      A1   20040115
         US 7125698          B2   20061024
AI       US 2002-264213      A1   20021003 (10)
RLI      Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,
         PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug
         2000, GRANTED, Pat. No. US 6544772
PRAI     US 1999-147853P       19990809 (60)
         US 1999-147852P       19990809 (60)
         US 1999-152032P       19990901 (60)
         US 1999-152031P       19990901 (60)
DT       Utility
FS       APPLICATION
LN.CNT 5375
INCL     INCLM: 435/006.000
         INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200
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NCL    NCLM:  435/193.000; 435/006.000
       NCLS:  426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;
              435/252.300; 435/320.100; 536/023.200
IC     [7]
       ICM    C12Q001-68
       ICS    C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335
       IPCI   C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
              C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];
              C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
       IPCI-2 C12N0009-10 [I,A]
       IPCR   C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C*];
              A23C0019-032 [I,A]; A61K0038-00 [N,C*]; A61K0038-00 [N,A];
              C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
              C12N0001-21 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5     ANSWER 19 OF 27  USPATFULL on STN
AN     2004:250212  USPATFULL
TI     Nucleic acid and amino acid sequences relating to Streptococcus
       pneumoniae for diagnostics and therapeutics
IN     Doucette-Stamm, Lynn A., Framingham, MA, United States
       Bush, David, Somerville, MA, United States
PA     Genome Therapeutics Corporation, Waltham, MA, United States (U.S.
       corporation)
PI     US 6800744        B1  20041005
AI     US 1998-107433        19980630 (9)
PRAI   US 1998-85131P    19980512 (60)
       US 1997-51553P    19970702 (60)
DT     Utility
FS     GRANTED
LN.CNT 11545
INCL   INCLM: 536/023.100
       INCLS: 435/006.000; 435/320.100; 435/325.000; 435/254.000; 435/419.000;
              536/024.100; 536/023.400; 536/024.320
NCL    NCLM:  536/023.100
       NCLS:  435/006.000; 435/320.100; 435/325.000; 435/419.000; 536/023.400;
              536/024.100; 536/024.320
IC     [7]
       ICM    C12Q001-68
       ICS    C12N001-14; C12N015-00; C12N005-00; C12N005-04; C07H021-02;
              C07H021-04
       IPCI   C12Q0001-68 [ICM,7]; C12N0001-14 [ICS,7]; C12N0015-00 [ICS,7];
              C12N0005-00 [ICS,7]; C12N0005-04 [ICS,7]; C07H0021-02 [ICS,7];
              C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]
       IPCR   C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
              C07K0014-195 [I,C*]; C07K0014-315 [I,A]
EXF    536/23.1; 536/23.4; 536/24.32; 435/320.1; 435/325; 435/254.11; 435/419;
       435/6
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5     ANSWER 20 OF 27  USPATFULL on STN
AN     2003:71519  USPATFULL
TI     Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN     Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
       Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
       Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
       Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
       Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
       Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF
       Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF
       Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF
PI     US 20030049804        A1  20030313
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AI       US 2000-746660        A1  20001222 (9)
RLI      Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
         PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun
         2000, PENDING
PRAI     DE 1999-19931420      19990708
         US 1999-141031P       19990625 (60)
         US 1999-142101P       19990702 (60)
         US 1999-148613P       19990812 (60)
         US 2000-187970P       20000309 (60)
DT       Utility
FS       APPLICATION
LN.CNT 15004
INCL     INCLM: 435/115.000
         INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200
NCL      NCLM:  435/115.000
         NCLS:  435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200
IC       [7]
         ICM    C12P013-08
         ICS    C07H021-04; C12N009-00; C12P021-02; C12N001-21
         IPCI   C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
                C07H0021-00 [ICS,7,C*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];
                C12N0001-21 [ICS,7]
         IPCR   C07K0014-195 [I,C*]; C07K0014-34 [I,A]; C12N0001-21 [I,C*];
                C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
                C12N0009-18 [I,C*]; C12N0009-18 [I,A]; C12N0009-90 [I,C*];
                C12N0009-90 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 17

L5    ANSWER 17 OF 27   USPATFULL on STN
AN       2004:95339   USPATFULL
TI       Nutritional formulations containing synbiotic substances
IN       Kaup, Susan M., Collingswood, NJ, UNITED STATES
         Wilson, Jeffrey L., Doylestown, PA, UNITED STATES
         Kostek, Beverley M., Glen Mills, PA, UNITED STATES
         Frantz, David C., Pottstown, PA, UNITED STATES
PA       Wyeth, Madison, NJ, UNITED STATES, 07940 (U.S. corporation)
PI       US 20040072794        A1  20040415
AI       US 2003-681658        A1  20031008 (10)
PRAI     US 2002-418109P       20021011 (60)
DT       Utility
FS       APPLICATION
LN.CNT 542
INCL     INCLM: 514/054.000
         INCLS: 424/093.450
NCL      NCLM:  514/054.000
         NCLS:  424/093.450
IC       [7]
         ICM    A61K045-00
         ICS    A61K031-715
         IPCI   A61K0045-00 [ICM,7]; A61K0031-715 [ICS,7]
         IPCR   A23L0001-052 [I,C*]; A23L0001-0528 [I,A]; A23L0001-29 [I,C*];
                A23L0001-29 [I,A]; A23L0001-30 [I,C*]; A23L0001-30 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 17 ab

L5    ANSWER 17 OF 27   USPATFULL on STN
AB       Nutritional compositions are provided which comprise oligofructose,
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sialyllactose and probiotic bacteria, which are useful in the
eradication of pathogenic microorganisms in the gastrointestinal tracts
of patients.

=> d l5 17 kwic

L5   ANSWER 17 OF 27   USPATFULL on STN
SUMM   [0004] Prebiotics are nondigestible food ingredients that that
        beneficially affect the host by selectively stimulating the growth
        and/or activity of one or a limited number. . .
SUMM   [0011] Sialyllactose is known to have anti-adhesive properties for
        specific pathogenic bacteria. For example, sialyllactose acts to inhibit
        cholera toxin invitro (Idota et al., "Inhibition of Cholera
        Toxin by Human Milk Fractions and Sialyllactose," Biosci.
        Biotech. Biochem. 59:417-419) and Helicobacter pylori (Simon et al.,
        "Inhibition of Helicobacter pylori Binding to Gastrointestinal
        Epithelial Cells by Sialic Acid-Containing Oligosaccharides," Infection
        and Immunity, 750-757, (1997)).
SUMM   [0015] Probiotics are live microbial food ingredients that
        have a beneficial effect on human health. (Salminen et al., "Functional
        food science and gastrointestinal physiology and function."
        Brit. J. Nutr. 80(suppl. 1):S147-S171 (1998)).
SUMM   . . . carbohydrate to lactic acid. The specific strains most often
        studied include members of the genera Lactobacillus and Bifidobacterium.
        (Sanders, "Probiotics." Food Technol. 53:67-77 (1999)).
SUMM   [0017] Some lactic acid bacteria specifically produce lactic acid as a
        major product of their metabolism. Some produce predominantly
        the levorotary "L"-form of lactic acid [L(+)-lactic acid], others
        produce predominantly the dextrorotary "D"-form. . .
SUMM   [0019] A milk product containing LGG significantly shortened
        the duration of diarrhea in young children. (Kaila et al., "Enhancement
        of the circulating antibody secreting. . .
SUMM   [0021] U.S. Pat. No. 5,908,646 discloses a method for inhibiting the
        growth or activity of Clostridium species in a human food
        product by adding an effective amount of the beneficial
        microorganism, L. rhamnosus [L. casei subspecies rhamnosus], which
        produces predominantly L(+)-lactic acid.
SUMM   . . . viable cells of three specific microorganisms beneficial to the
        human intestinal microorganisms for preventing diarrhea. Specifically,
        the three microorganisms are Lactobacillus reuteri,
        Lactobacillus acidophilus and Bifidobacterium infantis. The diarrhea can
        be caused by antibiotic treatment or by infection with a virus, a. . .
SUMM   . . . "Bifidobacterium bifidum." (Fukushima et al., "Effect of a
        probiotic formula on intestinal immunoglobulin A production in healthy
        children." Int. J. Food Microb. 42-39-44 (1998)).

=> d l5 18

L5   ANSWER 18 OF 27   USPATFULL on STN
AN   2004:12970 USPATFULL
TI   Polynucleotides, materials incorporating them, and methods for using
        them
IN   Glenn, Matthew, Whenuapai, NEW ZEALAND
        Havukkala, Ilkka J., Remuera, NEW ZEALAND
        Lubbers, Mark, Palmerston North, NEW ZEALAND
        Dekker, James, Palmerston North, NEW ZEALAND
PA   GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND
        (non-U.S. corporation)
PI   US 20040009490   A1   20040115
        US 7125698   B2   20061024

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AI       US 2002-264213        A1  20021003 (10)
RLI      Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,
         PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug
         2000, GRANTED, Pat. No. US 6544772
PRAI     US 1999-147853P       19990809 (60)
         US 1999-147852P       19990809 (60)
         US 1999-152032P       19990901 (60)
         US 1999-152031P       19990901 (60)
DT       Utility
FS       APPLICATION
LN.CNT 5375
INCL     INCLM: 435/006.000
         INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200
NCL      NCLM:  435/193.000; 435/006.000
         NCLS:  426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;
                435/252.300; 435/320.100; 536/023.200
IC       [7]
         ICM    C12Q001-68
         ICS    C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335
         IPCI   C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
                C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];
                C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C*]
         IPCI-2 C12N0009-10 [I,A]
         IPCR   C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C*];
                A23C0019-032 [I,A]; A61K0038-00 [N,C*]; A61K0038-00 [N,A];
                C07K0014-195 [I,C*]; C07K0014-335 [I,A]; C12N0001-21 [I,C*];
                C12N0001-21 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 19

L5       ANSWER 19 OF 27  USPATFULL on STN
AN       2004:250212  USPATFULL
TI       Nucleic acid and amino acid sequences relating to Streptococcus
         pneumoniae for diagnostics and therapeutics
IN       Doucette-Stamm, Lynn A., Framingham, MA, United States
         Bush, David, Somerville, MA, United States
PA       Genome Therapeutics Corporation, Waltham, MA, United States (U.S.
         corporation)
PI       US 6800744            B1  20041005
AI       US 1998-107433           19980630 (9)
PRAI     US 1998-85131P        19980512 (60)
         US 1997-51553P        19970702 (60)
DT       Utility
FS       GRANTED
LN.CNT 11545
INCL     INCLM: 536/023.100
         INCLS: 435/006.000; 435/320.100; 435/325.000; 435/254.000; 435/419.000;
                536/024.100; 536/023.400; 536/024.320
NCL      NCLM:  536/023.100
         NCLS:  435/006.000; 435/320.100; 435/325.000; 435/419.000; 536/023.400;
                536/024.100; 536/024.320
IC       [7]
         ICM    C12Q001-68
         ICS    C12N001-14; C12N015-00; C12N005-00; C12N005-04; C07H021-02;
                C07H021-04
         IPCI   C12Q0001-68 [ICM,7]; C12N0001-14 [ICS,7]; C12N0015-00 [ICS,7];
                C12N0005-00 [ICS,7]; C12N0005-04 [ICS,7]; C07H0021-02 [ICS,7];
                C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]
         IPCR   C07H0021-00 [I,C*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];
                C07K0014-195 [I,C*]; C07K0014-315 [I,A]
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EXF    536/23.1; 536/23.4; 536/24.32; 435/320.1; 435/325; 435/254.11; 435/419;
       435/6
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 20-28

L5    ANSWER 20 OF 27  USPATFULL on STN
AN       2003:71519  USPATFULL
TI       Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN       Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
         Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
         Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
         Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
         Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
         Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF
         Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF
         Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF
PI       US 20030049804     A1 20030313
AI       US 2000-746660     A1 20001222 (9)
RLI      Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
         PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun
         2000, PENDING
PRAI     DE 1999-19931420     19990708
         US 1999-141031P      19990625 (60)
         US 1999-142101P      19990702 (60)
         US 1999-148613P      19990812 (60)
         US 2000-187970P      20000309 (60)
DT       Utility
FS       APPLICATION
LN.CNT 15004
INCL     INCLM: 435/115.000
         INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200
NCL      NCLM:  435/115.000
         NCLS:  435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200
IC       [7]
         ICM    C12P013-08
         ICS    C07H021-04; C12N009-00; C12P021-02; C12N001-21
         IPCI   C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
                C07H0021-00 [ICS,7,C*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];
                C12N0001-21 [ICS,7]
         IPCR   C07K0014-195 [I,C*]; C07K0014-34 [I,A]; C12N0001-21 [I,C*];
                C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
                C12N0009-18 [I,C*]; C12N0009-18 [I,A]; C12N0009-90 [I,C*];
                C12N0009-90 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5    ANSWER 21 OF 27  USPATFULL on STN
AN       2003:95966  USPATFULL
TI       Polynucleotides, materials incorporating them, and methods for using
         them
IN       Glenn, Matthew, Auckland, NEW ZEALAND
         Havukkala, Ilkka J., Auckland, NEW ZEALAND
         Bloksberg, Leonard N., Auckland, NEW ZEALAND
         Lubbers, Mark W., Palmerston North, NEW ZEALAND
         Dekker, James, Palmerston North, NEW ZEALAND
         Christensson, Anna C., Lund, SWEDEN
         Holland, Ross, Palmerson North, NEW ZEALAND
         O'Toole, Paul W., Palmerston North, NEW ZEALAND
         Reid, Julian R., Palmerston North, NEW ZEALAND
         Coolbear, Timothy, Palmerston North, NEW ZEALAND
PA       Genesis Research & Development Corp. Ltd, Parnell, NEW ZEALAND (non-U.S.
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          corporation)
          Via Lachia Bioscience (NZ) Ltd., Auckland, NEW ZEALAND (non-U.S.
          corporation)
PI     US 6544772        B1   20030408
AI     US 2000-634238         20000808 (9)
DT     Utility
FS     GRANTED
LN.CNT 2015
INCL   INCLM: 435/252.300
       INCLS: 435/320.100; 536/023.700
NCL    NCLM:  435/252.300
       NCLS:  435/320.100; 536/023.700
IC     [7]
       ICM    C12N001-21
       ICS    C12N015-63; C12N015-31
       IPCI   C12N0001-21 [ICM,7]; C12N0015-63 [ICS,7]; C12N0015-31 [ICS,7]
       IPCR   A23C0019-00 [I,C*]; A23C0019-032 [I,A]; C07K0014-195 [I,C*];
              C07K0014-335 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
              C12N0015-31 [I,C*]; C12N0015-31 [I,A]
EXF    435/252.3; 435/320.1; 536/23.7
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


L5     ANSWER 22 OF 27  BIOTECHDS COPYRIGHT 2008 THOMSON REUTERS on STN
AN     1999-00562  BIOTECHDS
TI     Use of lactic and propionic acid bacteria;
          to bind mycotoxin to prevent their absorption or to purify
          contaminated food or feedstuff
AU     El-Nezami H; Kankaanpaa P; Salminen S; Ahokas J
PA     Roy.Melbourne-Inst.Technol.
LO     Melbourne, Victoria, Australia.
PI     WO 9834503 13 Aug 1998
AI     WO 1998-AU63 6 Feb 1998
PRAI   AU 1997-5005 7 Feb 1997
DT     Patent
LA     English
OS     WPI: 1998-557001 [49]


L5     ANSWER 23 OF 27     GENBANK®  COPYRIGHT 2008 on STN

LOCUS (LOC):            CP000705     GenBank (R)
GenBank ACC. NO. (GBN): CP000705 AAOV01000000 AAOV01000001-AAOV01000097
GenBank VERSION (VER):  CP000705.1  GI:148530277
SEQUENCE LENGTH (SQL):  1999618
MOLECULE TYPE (CI):     DNA; circular
DIVISION CODE (CI):     Bacteria
DATE (DATE):            17 Oct 2007
DEFINITION (DEF):       Lactobacillus reuteri F275,
                        complete genome.
SOURCE:                 Lactobacillus reuteri F275
 ORGANISM (ORGN):       Lactobacillus reuteri F275
                        Bacteria; Firmicutes; Lactobacillales;
                        Lactobacillaceae; Lactobacillus
PROJECT (PJID):         GenomeProject:15766
COMMENT:
       URL -- http://www.jgi.doe.gov
       JGI Project ID: 4000135
       Source DNA available from Gerald Tannock
       (gerald.tannock@stonebow.otago.ac.nz)
       Bacteria available from DSMZ: DSM 20016
       Contacts: Gerald Tannock (gerald.tannock@stonebow.otago.ac.nz)
                 Paul Richardson (microbes@cuba.jgi-psf.org)
       Quality assurance done by JGI-Stanford
```

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     Annotation done by JGI-ORNL and JGI-PGF
     Finishing done by JGI-PGF
     Finished microbial genomes have been curated to close all gaps with
     greater than 98% coverage of at least two independent clones. Each
     base pair has a minimum q (quality) value of 30 and the total error
     rate is less than one per 50000.
     The JGI and collaborators endorse the principles for the
     distribution and use of large scale sequencing data adopted by the
     larger genome sequencing community and urge users of this data to
     follow them. It is our intention to publish the work of this
     project in a timely fashion and we welcome collaborative
     interaction on the project and analysis.
     (http://www.genome.gov/page.cfm?pageID=10506376).
REFERENCE:              1  (bases 1 to 1999618)
   AUTHOR (AU):         Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;
                        Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;
                        Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;
                        Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;
                        Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.
   TITLE (TI):          Complete sequence of chromosome of
                        Lactobacillus reuteri DSM 20016
   JOURNAL (SO):        Unpublished
REFERENCE:              2  (bases 1 to 1999618)
   AUTHOR (AU):         Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;
                        Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;
                        Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;
                        Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;
                        Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.
   TITLE (TI):          Direct Submission
   JOURNAL (SO):        Submitted (17-MAY-2007) US DOE Joint Genome Institute,
                        2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698,
                        USA


FEATURES (FEAT):
   Feature Key     Location              Qualifier
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source          1..1999618            /organism="Lactobacillus reuteri
                                       F275"
                                       /mol-type="genomic DNA"
                                       /strain="DSM 20016"
                                       /db-xref="taxon:299033"
                                       /note="F275 = DSM 20016 = JCM
                                       1112"



L5   ANSWER 24 OF 27      GENBANK®  COPYRIGHT 2008 on STN

LOCUS (LOC):             AM270397      GenBank (R)
GenBank ACC. NO. (GBN):  AM270397
GenBank VERSION (VER):   AM270397.1  GI:134084136
CAS REGISTRY NO. (RN):   928607-03-8
SEQUENCE LENGTH (SQL):   163680
MOLECULE TYPE (CI):      DNA; linear
DIVISION CODE (CI):      Plants, fungi, algae
DATE (DATE):             24 Mar 2007
DEFINITION (DEF):        Aspergillus niger contig An18c0040, complete genome.
SOURCE:                  Aspergillus niger
 ORGANISM (ORGN):        Aspergillus niger
                         Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                         Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic
                         Trichocomaceae; Aspergillus
REFERENCE:               1  (bases 150631 to 153085)
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AUTHOR (AU):          Habison,A.; Kubicek,C.P.; Rohr,M.
TITLE (TI):           Partial purification and regulatory properties of
                      phosphofructokinase from Aspergillus niger
JOURNAL (SO):         Biochem. J., 209 (3), 669-676 (1983)
OTHER SOURCE (OS):    CA 99:171737
REFERENCE:            2  (bases 71863 to 73356)
AUTHOR (AU):          Manney,T.R.
TITLE (TI):           Expression of the BAR1 gene in Saccharomyces
                      cerevisiae: induction by the alpha mating pheromone of
                      an activity associated with a secreted protein
JOURNAL (SO):         J. Bacteriol., 155 (1), 291-301 (1983)
OTHER SOURCE (OS):    CA 99:102121
REFERENCE:            3  (bases 71863 to 73356)
AUTHOR (AU):          Jones,E.W.
TITLE (TI):           The synthesis and function of proteases in
                      Saccharomyces: genetic approaches
JOURNAL (SO):         Annu. Rev. Genet., 18, 233-270 (1984)
OTHER SOURCE (OS):    CA 102:92538
REFERENCE:            4  (bases 144032 to 145578)
AUTHOR (AU):          Brandsch,R.; Bichler,V.
TITLE (TI):           In vivo and in vitro expression of the
                      6-hydroxy-D-nicotine oxidase gene of Arthrobacter
                      oxidans, cloned into Escherichia coli, as an
                      enzymatically active, covalently flavinylated
                      polypeptide
JOURNAL (SO):         FEBS Lett., 192 (2), 204-208 (1985)
OTHER SOURCE (OS):    CA 104:29597
REFERENCE:            5  (bases 150631 to 153085)
AUTHOR (AU):          Schreferl,G.; Kubicek,C.P.; Rohr,M.
TITLE (TI):           Inhibition of citric acid accumulation by manganese
                      ions in Aspergillus niger mutants with reduced citrate
                      control of phosphofructokinase
JOURNAL (SO):         J. Bacteriol., 165 (3), 1019-1022 (1986)
OTHER SOURCE (OS):    CA 104:165023
REFERENCE:            6  (bases 156827 to 158638)
AUTHOR (AU):          Whittington,H.A.; Grant,S.; Roberts,C.F.; Lamb,H.;
                      Hawkins,A.R.
TITLE (TI):           Identification and isolation of a putative permease
                      gene in the quinic acid utilization (QUT) gene cluster
                      of Aspergillus nidulans
JOURNAL (SO):         Curr. Genet., 12 (2), 135-139 (1987)
OTHER SOURCE (OS):    CA 107:91128
REFERENCE:            7  (bases 54105 to 55762)
AUTHOR (AU):          Chisholm,V.T.; Lea,H.Z.; Rai,R.; Cooper,T.G.
TITLE (TI):           Regulation of allantoate transport in wild-type and
                      mutant strains of Saccharomyces cerevisiae
JOURNAL (SO):         J. Bacteriol., 169 (4), 1684-1690 (1987)
OTHER SOURCE (OS):    CA 106:172689
REFERENCE:            8  (bases 71863 to 73356)
AUTHOR (AU):          MacKay,V.L.; Welch,S.K.; Insley,M.Y.; Manney,T.R.;
                      Holly,J.; Saari,G.C.; Parker,M.L.
TITLE (TI):           The Saccharomyces cerevisiae BAR1 gene encodes an
                      exported protein with homology to pepsin
JOURNAL (SO):         Proc. Natl. Acad. Sci. U.S.A., 85 (1), 55-59 (1988)
OTHER SOURCE (OS):    CA 108:125658
REFERENCE:            9  (bases 54105 to 55762)
AUTHOR (AU):          Rai,R.; Genbauffe,F.S.; Cooper,T.G.
TITLE (TI):           Structure and transcription of the allantoate permease
                      gene (DAL5) from Saccharomyces cerevisiae
JOURNAL (SO):         J. Bacteriol., 170 (1), 266-271 (1988)
OTHER SOURCE (OS):    CA 109:17930
REFERENCE:            10
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AUTHOR (AU):        Hawkins,A.R.; Lamb,H.K.; Smith,M.; Keyte,J.W.;
                    Roberts,C.F.
TITLE (TI):         Molecular organisation of the quinic acid utilization
                    (QUT) gene cluster in Aspergillus nidulans
JOURNAL (SO):       Mol. Gen. Genet., 214 (2), 224-231 (1988)
OTHER SOURCE (OS):  CA 111:188522
REFERENCE:          11 (bases 68231 to 69040)
AUTHOR (AU):        Honjo,M.; Nakayama,A.; Fukazawa,K.; Kawamura,K.;
                    Ando,K.; Furutani,Y.
TITLE (TI):         A novel Bacillus subtilis gene involved in negative
                    control of sporulation and degradative-enzyme
                    production
JOURNAL (SO):       J. Bacteriol., 172 (4), 1783-1790 (1990)
OTHER SOURCE (OS):  CA 113:146166
REFERENCE:          12 (bases 5212 to 7379)
AUTHOR (AU):        Nikawa,J.; Hosaka,K.; Tsukagoshi,Y.; Yamashita,S.
TITLE (TI):         Primary structure of the yeast choline transport gene
                    and regulation of its expression
JOURNAL (SO):       J. Biol. Chem., 265 (26), 15996-16003 (1990)
OTHER SOURCE (OS):  CA 114:18549
REFERENCE:          13 (bases 159975 to 161849)
AUTHOR (AU):        Fling,M.E.; Kopf,J.; Tamarkin,A.; Gorman,J.A.;
                    Smith,H.A.; Koltin,Y.
TITLE (TI):         Analysis of a Candida albicans gene that encodes a
                    novel mechanism for resistance to benomyl and
                    methotrexate
JOURNAL (SO):       Mol. Gen. Genet., 227 (2), 318-329 (1991)
OTHER SOURCE (OS):  CA 116:100405
REFERENCE:          14 (bases 28874 to 30837)
AUTHOR (AU):        Masuda,N.; Kitamura,N.; Saito,K.
TITLE (TI):         Primary structure of protein moiety of Penicillium
                    notatum phospholipase B deduced from the cDNA
JOURNAL (SO):       Eur. J. Biochem., 202 (3), 783-787 (1991)
OTHER SOURCE (OS):  CA 118:76020
REFERENCE:          15 (bases 100363 to 101496)
AUTHOR (AU):        Sakoda,H.; Imanaka,T.
TITLE (TI):         Cloning and sequencing of the gene coding for alcohol
                    dehydrogenase of Bacillus stearothermophilus and
                    rational shift of the optimum pH
JOURNAL (SO):       J. Bacteriol., 174 (4), 1397-1402 (1992)
OTHER SOURCE (OS):  CA 118:186708
REFERENCE:          16 (bases 20773 to 22555)
AUTHOR (AU):        Kamoda,S.; Saburi,Y.
TITLE (TI):         Structural and enzymatical comparison of
                    lignostilbene-alpha,beta-dioxygenase isozymes, I, II,
                    and III, from Pseudomonas paucimobilis TMY1009
JOURNAL (SO):       Biosci. Biotechnol. Biochem., 57 (6), 931-934 (1993)
OTHER SOURCE (OS):  CA 119:154577
REFERENCE:          17 (bases 80602 to 83154)
AUTHOR (AU):        ElBerry,H.M.; Majumdar,M.L.; Cunningham,T.S.;
                    Sumrada,R.A.; Cooper,T.G.
TITLE (TI):         Regulation of the urea active transporter gene (DUR3)
                    in Saccharomyces cerevisiae
JOURNAL (SO):       J. Bacteriol., 175 (15), 4688-4698 (1993)
OTHER SOURCE (OS):  CA 119:242524
REFERENCE:          18 (bases 23096 to 24052)
AUTHOR (AU):        Roper,D.I.; Cooper,R.A.
TITLE (TI):         Purification, nucleotide sequence and some properties
                    of a bifunctional isomerase/decarboxylase from the
                    homoprotocatechuate degradative pathway of Escherichia
                    coli C
JOURNAL (SO):       Eur. J. Biochem., 217 (2), 575-580 (1993)
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   OTHER SOURCE (OS):    CA 119:265270
REFERENCE:               19 (bases 5212 to 7379)
   AUTHOR (AU):          Li,Z.; Brendel,M.
   TITLE (TI):           Co-regulation with genes of phospholipid biosynthesis
                         of the CTR/HNM1-encoded choline/nitrogen mustard
                         permease in Saccharomyces cerevisiae
   JOURNAL (SO):         Mol. Gen. Genet., 241 (5-6), 680-684 (1993)
   OTHER SOURCE (OS):    CA 121:28475
REFERENCE:               20 (bases 159975 to 161849)
   AUTHOR (AU):          Ben-Yaacov,R.; Knoller,S.; Caldwell,G.A.; Becker,J.M.;
                         Koltin,Y.
   TITLE (TI):           Candida albicans gene encoding resistance to benomyl
                         and methotrexate is a multidrug resistance gene
   JOURNAL (SO):         Antimicrob. Agents Chemother., 38 (4), 648-652 (1994)
   OTHER SOURCE (OS):    CA 121:2236
REFERENCE:               21 (bases 150631 to 153085)
   AUTHOR (AU):          Legisa,M.; Bencina,M.
   TITLE (TI):           Evidence for the activation of 6-phosphofructo-1-kinase
                         by cAMP-dependent protein kinase in Aspergillus niger
   JOURNAL (SO):         FEMS Microbiol. Lett., 118 (3), 327-333 (1994)
   OTHER SOURCE (OS):    CA 121:102759
REFERENCE:               22 (bases 138020 to 140061)
   AUTHOR (AU):          Kim,Y.J.; Bjorklund,S.; Li,Y.; Sayre,M.H.;
                         Kornberg,R.D.
   TITLE (TI):           A multiprotein mediator of transcriptional activation
                         and its interaction with the C-terminal repeat domain
                         of RNA polymerase II
   JOURNAL (SO):         Cell, 77 (4), 599-608 (1994)
   OTHER SOURCE (OS):    CA 121:102149
REFERENCE:               23 (bases 38805 to 39836)
   AUTHOR (AU):          Downs,D.M.; Petersen,L.
   TITLE (TI):           apbA, a new genetic locus involved in thiamine
                         biosynthesis in Salmonella typhimurium
   JOURNAL (SO):         J. Bacteriol., 176 (16), 4858-4864 (1994)
   OTHER SOURCE (OS):    CA 121:197350
REFERENCE:               24 (bases 5212 to 7379)
   AUTHOR (AU):          Li,Z.; Brendel,M.
   TITLE (TI):           Sensitivity to nitrogen mustard in Saccharomyces
                         cerevisiae is independently determined by regulated
                         choline permease and DNA repair
   JOURNAL (SO):         Mutat. Res., 315 (2), 139-145 (1994)
   OTHER SOURCE (OS):    CA 121:198201
REFERENCE:               25 (bases 85096 to 90863)
   AUTHOR (AU):          Szczypka,M.S.; Wemmie,J.A.; Moye-Rowley,W.S.;
                         Thiele,D.J.
   TITLE (TI):           A yeast metal resistance protein similar to human
                         cystic fibrosis transmembrane conductance regulator
                         (CFTR) and multidrug resistance-associated protein
   JOURNAL (SO):         J. Biol. Chem., 269 (36), 22853-22857 (1994)
   OTHER SOURCE (OS):    CA 122:26140
REFERENCE:               26 (bases 91484 to 93088)
   AUTHOR (AU):          Knight,S.A.; Tamai,K.T.; Kosman,D.J.; Thiele,D.J.
   TITLE (TI):           Identification and analysis of a Saccharomyces
                         cerevisiae copper homeostasis gene encoding a
                         homeodomain protein
   JOURNAL (SO):         Mol. Cell. Biol., 14 (12), 7792-7804 (1994)
   OTHER SOURCE (OS):    CA 122:73697
REFERENCE:               27 (bases 85096 to 90863)
   AUTHOR (AU):          Wemmie,J.A.; Szczypka,M.S.; Thiele,D.J.;
                         Moye-Rowley,W.S.
   TITLE (TI):           Cadmium tolerance mediated by the yeast AP-1 protein
                         requires the presence of an ATP-binding cassette
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                                    transporter-encoding gene, YCF1
      JOURNAL (SO):                 J. Biol. Chem., 269 (51), 32592-32597 (1994)
      OTHER SOURCE (OS):            CA 121:294343
   REFERENCE:                       28 (bases 20773 to 22555)
      AUTHOR (AU):                  Kamoda,S.; Saburi,Y.
      TITLE (TI):                   Cloning of a lignostilbene-alpha,beta-dioxygenase
                                    isozyme gene from Pseudomonas paucimobilis TMY1009
      JOURNAL (SO):                 Biosci. Biotechnol. Biochem., 59 (10), 1866-1868 (1995)
      OTHER SOURCE (OS):            CA 124:47043
   REFERENCE:                       29 (bases 85096 to 90863)
      AUTHOR (AU):                  Li,Z.S.; Szczypka,M.; Lu,Y.P.; Thiele,D.J.; Rea,P.A.
      TITLE (TI):                   The yeast cadmium factor protein (YCF1) is a vacuolar
                                    glutathione S-conjugate pump
      JOURNAL (SO):                 J. Biol. Chem., 271 (11), 6509-6517 (1996)
      OTHER SOURCE (OS):            CA 124:226108
   REFERENCE:                       30 (bases 33419 to 35477)
      AUTHOR (AU):                  Silva,J.C.; Minto,R.E.; Barry,C.E. III; Holland,K.A.;
                                    Townsend,C.A.
      TITLE (TI):                   Isolation and characterization of the versicolorin B
                                    synthase gene from Aspergillus parasiticus. Expansion
                                    of the aflatoxin b1 biosynthetic gene cluster
      JOURNAL (SO):                 J. Biol. Chem., 271 (23), 13600-13608 (1996)
      OTHER SOURCE (OS):            CA 125:50401
   REFERENCE:                       31 (bases 15614 to 17392)
      AUTHOR (AU):                  Covert,S.F.; Enkerli,J.; Miao,V.P.; VanEtten,H.D.
      TITLE (TI):                   A gene for maackiain detoxification from a dispensable
                                    chromosome of Nectria haematococca
      JOURNAL (SO):                 Mol. Gen. Genet., 251 (4), 397-406 (1996)
      OTHER SOURCE (OS):            CA 125:106677
   REFERENCE:                       32 (bases 131646 to 132375)
      AUTHOR (AU):                  Mitsuhashi,S.; Miyachi,S.
      TITLE (TI):                   Amino acid sequence homology between N- and C-terminal
                                    halves of a carbonic anhydrase in Porphyridium
                                    purpureum, as deduced from the cloned cDNA
      JOURNAL (SO):                 J. Biol. Chem., 271 (45), 28703-28709 (1996)
      OTHER SOURCE (OS):            CA 125:321312
   REFERENCE:                       33 (bases 85096 to 90863)
      AUTHOR (AU):                  Li,Z.S.; Lu,Y.P.; Zhen,R.G.; Szczypka,M.; Thiele,D.J.;
                                    Rea,P.A.
      TITLE (TI):                   A new pathway for vacuolar cadmium sequestration in
                                    Saccharomyces cerevisiae: YCF1-catalyzed transport of
                                    bis(glutathionato)cadmium
      JOURNAL (SO):                 Proc. Natl. Acad. Sci. U.S.A., 94 (1), 42-47 (1997)
      OTHER SOURCE (OS):            CA 126:127966
   REFERENCE:                       34 (bases 1241 to 3043)
      AUTHOR (AU):                  Saito,Y.; Ishii,Y.; Hayashi,H.; Imao,Y.; Akashi,T.;
                                    Yoshikawa,K.; Noguchi,Y.; Soeda,S.; Yoshida,M.;
                                    Niwa,M.; Hosoda,J.; Shimomura,K.
      TITLE (TI):                   Cloning of genes coding for L-sorbose and L-sorbosone
                                    dehydrogenases from Gluconobacter oxydans and microbial
                                    production of 2-keto-L-gulonate, a precursor of
                                    L-ascorbic acid, in a recombinant G. oxydans strain
      JOURNAL (SO):                 Appl. Environ. Microbiol., 63 (2), 454-460 (1997)
      OTHER SOURCE (OS):            CA 126:167180
   REFERENCE:                       35 (bases 150631 to 153085)
      AUTHOR (AU):                  Ruijter,G.J.; Panneman,H.; Visser,J.
      TITLE (TI):                   Overexpression of phosphofructokinase and pyruvate
                                    kinase in citric acid-producing Aspergillus niger
      JOURNAL (SO):                 Biochim. Biophys. Acta, 1334 (2-3), 317-326 (1997)
      OTHER SOURCE (OS):            CA 126:222695
   REFERENCE:                       36 (bases 49850 to 51919)
      AUTHOR (AU):                  Prieto,R.; Woloshuk,C.P.
```

TITLE (TI):   ord1, an oxidoreductase gene responsible for conversion
                       of O-methylsterigmatocystin to aflatoxin in Aspergillus
                       flavus
JOURNAL (SO):   Appl. Environ. Microbiol., 63 (5), 1661-1666 (1997)
OTHER SOURCE (OS):   CA 127:13942
REFERENCE: 37 (bases 17766 to 20491)
AUTHOR (AU):   Todd,R.B.; Murphy,R.L.; Martin,H.M.; Sharp,J.A.;
                       Davis,M.A.; Katz,M.E.; Hynes,M.J.
TITLE (TI):   The acetate regulatory gene facB of Aspergillus
                       nidulans encodes a Zn(II)2Cys6 transcriptional
                       activator
JOURNAL (SO):   Mol. Gen. Genet., 254 (5), 495-504 (1997)
OTHER SOURCE (OS):   CA 127:105007
REFERENCE: 38 (bases 71863 to 73356)
AUTHOR (AU):   Ballensiefen,W.; Schmitt,H.D.
TITLE (TI):   Periplasmic Bar1 protease of Saccharomyces cerevisiae
                       is active before reaching its extracellular destination
JOURNAL (SO):   Eur. J. Biochem., 247 (1), 142-147 (1997)
OTHER SOURCE (OS):   CA 127:187926
REFERENCE: 39 (bases 52148 to 53720)
AUTHOR (AU):   Kuroyanagi,N.; Onogi,H.; Wakabayashi,T.; Hagiwara,M.
TITLE (TI):   Novel SR-protein-specific kinase, SRPK2, disassembles
                       nuclear speckles
JOURNAL (SO):   Biochem. Biophys. Res. Commun., 242 (2), 357-364 (1998)
OTHER SOURCE (OS):   CA 128:241040
REFERENCE: 40 (bases 113565 to 114733)
AUTHOR (AU):   MacDiarmid,C.W.; Gardner,R.C.
TITLE (TI):   Overexpression of the Saccharomyces cerevisiae
                       magnesium transport system confers resistance to
                       aluminum ion
JOURNAL (SO):   J. Biol. Chem., 273 (3), 1727-1732 (1998)
OTHER SOURCE (OS):   CA 128:177021
REFERENCE: 41 (bases 135940 to 137166)
AUTHOR (AU):   Wang,H.Y.; Lin,W.; Dyck,J.A.; Yeakley,J.M.;
                       Songyang,Z.; Cantley,L.C.; Fu,X.D.
TITLE (TI):   SRPK2: a differentially expressed SR protein-specific
                       kinase involved in mediating the interaction and
                       localization of pre-mRNA splicing factors in mammalian
                       cells
JOURNAL (SO):   J. Cell Biol., 140 (4), 737-750 (1998)
OTHER SOURCE (OS):   CA 128:306636
REFERENCE: 42 (bases 38805 to 39836)
AUTHOR (AU):   Frodyma,M.E.; Downs,D.
TITLE (TI):   ApbA, the ketopantoate reductase enzyme of Salmonella
                       typhimurium is required for the synthesis of thiamine
                       via the alternative pyrimidine biosynthetic pathway
JOURNAL (SO):   J. Biol. Chem., 273 (10), 5572-5576 (1998)
OTHER SOURCE (OS):   CA 128:305459
REFERENCE: 43 (bases 106231 to 106803)
AUTHOR (AU):   Woloshuk,C.P.; Prieto,R.
TITLE (TI):   Genetic organization and function of the aflatoxin B1
                       biosynthetic genes
JOURNAL (SO):   FEMS Microbiol. Lett., 160 (2), 169-176 (1998)
OTHER SOURCE (OS):   CA 128:290649
REFERENCE: 44 (bases 93571 to 94963)
AUTHOR (AU):   Philp,N.J.; Yoon,H.; Grollman,E.F.
TITLE (TI):   Monocarboxylate transporter MCT1 is located in the
                       apical membrane and MCT3 in the basal membrane of rat
                       RPE
JOURNAL (SO):   Am. J. Physiol., 274 (6 PT 2), R1824-R1828 (1998)
OTHER SOURCE (OS):   CA 129:159493
REFERENCE: 45 (bases 93571 to 94963)

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AUTHOR (AU):          Wilson,M.C.; Jackson,V.N.; Heddle,C.; Price,N.T.;
                      Pilegaard,H.; Juel,C.; Bonen,A.; Montgomery,I.;
                      Hutter,O.F.; Halestrap,A.P.
TITLE (TI):           Lactic acid efflux from white skeletal muscle is
                      catalyzed by the monocarboxylate transporter isoform
                      MCT3
JOURNAL (SO):         J. Biol. Chem., 273 (26), 15920-15926 (1998)
OTHER SOURCE (OS):    CA 129:159801
REFERENCE:            46 (bases 153410 to 154508)
AUTHOR (AU):          Dekkers,L.C.; van der Bij,A.J.; Mulders,I.H.;
                      Phoelich,C.C.; Wentwoord,R.A.; Glandorf,D.C.;
                      Wijffelman,C.A.; Lugtenberg,B.J.
TITLE (TI):           Role of the O-antigen of lipopolysaccharide, and
                      possible roles of growth rate and of NADH:ubiquinone
                      oxidoreductase (nuo) in competitive tomato root-tip
                      colonization by Pseudomonas fluorescens WCS365
JOURNAL (SO):         Mol. Plant Microbe Interact., 11 (8), 763-771 (1998)
OTHER SOURCE (OS):    CA 129:200426
REFERENCE:            47 (bases 146433 to 148685)
AUTHOR (AU):          Saito,K.; Yamazaki,H.; Ohnishi,Y.; Fujimoto,S.;
                      Takahashi,E.; Horinouchi,S.
TITLE (TI):           Production of trehalose synthase from a basidiomycete,
                      Grifola frondosa, in Escherichia coli
JOURNAL (SO):         Appl. Microbiol. Biotechnol., 50 (2), 193-198 (1998)
OTHER SOURCE (OS):    CA 130:956
REFERENCE:            48 (bases 122486 to 123895)
AUTHOR (AU):          Kimura,M.; Matsumoto,G.; Shingu,Y.; Yoneyama,K.;
                      Yamaguchi,I.
TITLE (TI):           The mystery of the trichothecene 3-O-acetyltransferase
                      gene. Analysis of the region around Tri101 and
                      characterization of its homologue from Fusarium
                      sporotrichioides
JOURNAL (SO):         FEBS Lett., 435 (2-3), 163-168 (1998)
OTHER SOURCE (OS):    CA 130:11163
REFERENCE:            49 (bases 146433 to 148685)
AUTHOR (AU):          Saito,K.; Kase,T.; Takahashi,E.; Horinouchi,S.
TITLE (TI):           Purification and characterization of a trehalose
                      synthase from the basidiomycete grifola frondosa
JOURNAL (SO):         Appl. Environ. Microbiol., 64 (11), 4340-4345 (1998)
OTHER SOURCE (OS):    CA 130:34870
REFERENCE:            50 (bases 14029 to 15172)
AUTHOR (AU):          Feng,Y.; Khoo,H.E.; Poh,C.L.
TITLE (TI):           Purification and characterization of gentisate
                      1,2-dioxygenases from Pseudomonas alcaligenes NCIB 9867
                      and Pseudomonas putida NCIB 9869
JOURNAL (SO):         Appl. Environ. Microbiol., 65 (3), 946-950 (1999)
OTHER SOURCE (OS):    CA 130:322223
REFERENCE:            51 (bases 59070 to 60560)
AUTHOR (AU):          Bosch,R.; Moore,E.R.; Garcia-Valdes,E.; Pieper,D.H.
TITLE (TI):           NahW, a novel, inducible salicylate hydroxylase
                      involved in mineralization of naphthalene by
                      Pseudomonas stutzeri AN10
JOURNAL (SO):         J. Bacteriol., 181 (8), 2315-2322 (1999)
OTHER SOURCE (OS):    CA 131:70144
REFERENCE:            52
AUTHOR (AU):          DeZwaan,T.M.; Carroll,A.M.; Valent,B.; Sweigard,J.A.
TITLE (TI):           Magnaporthe grisea pth11p is a novel plasma membrane
                      protein that mediates appressorium differentiation in
                      response to inductive substrate cues
JOURNAL (SO):         Plant Cell, 11 (10), 2013-2030 (1999)
OTHER SOURCE (OS):    CA 132:47358
REFERENCE:            53 (bases 122486 to 123895)
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AUTHOR (AU):            McCormick,S.P.; Alexander,N.J.; Trapp,S.E.; Hohn,T.M.
TITLE (TI):             Disruption of TRI101, the gene encoding trichothecene
                        3-O-acetyltransferase, from Fusarium sporotrichioides
JOURNAL (SO):           Appl. Environ. Microbiol., 65 (12), 5252-5256 (1999)
OTHER SOURCE (OS):      CA 132:118174
REFERENCE:              54 (bases 111907 to 113460)
AUTHOR (AU):            Muraguchi,H.; Kamada,T.
TITLE (TI):             A mutation in the eln2 gene encoding a cytochrome P450
                        of Coprinus cinereus affects mushroom morphogenesis
JOURNAL (SO):           Fungal Genet. Biol., 29 (1), 49-59 (2000)
OTHER SOURCE (OS):      CA 134:96073
REFERENCE:              55 (bases 108826 to 111209)
AUTHOR (AU):            Yu,J.; Chang,P.K.; Bhatnagar,D.; Cleveland,T.E.
TITLE (TI):             Genes encoding cytochrome P450 and monooxygenase
                        enzymes define one end of the aflatoxin pathway gene
                        cluster in Aspergillus parasiticus
JOURNAL (SO):           Appl. Microbiol. Biotechnol., 53 (5), 583-590 (2000)
OTHER SOURCE (OS):      CA 133:291807
REFERENCE:              56 (bases 122486 to 123895)
AUTHOR (AU):            Muhitch,M.J.; McCormick,S.P.; Alexander,N.J.; Hohn,T.M.
TITLE (TI):             Transgenic expression of the TRI101 or PDR5 gene
                        increases resistance of tobacco to the phytotoxic
                        effects of the trichothecene 4,15-diacetoxyscirpenol
JOURNAL (SO):           Plant Sci., 157 (2), 201-207 (2000)
OTHER SOURCE (OS):      CA 133:306551
REFERENCE:              57 (bases 107279 to 108340)
AUTHOR (AU):            Cheng,Q.; Thomas,S.M.; Kostichka,K.; Valentine,J.R.;
                        Nagarajan,V.
TITLE (TI):             Genetic analysis of a gene cluster for cyclohexanol
                        oxidation in Acinetobacter sp. Strain SE19 by in vitro
                        transposition
JOURNAL (SO):           J. Bacteriol., 182 (17), 4744-4751 (2000)
OTHER SOURCE (OS):      CA 134:37832
REFERENCE:              58 (bases 100363 to 101496)
AUTHOR (AU):            Jornvall,H.; Hoog,J.O.; Persson,B.; Pares,X.
TITLE (TI):             Pharmacogenetics of the alcohol dehydrogenase system
JOURNAL (SO):           Pharmacology, 61 (3), 184-191 (2000)
OTHER SOURCE (OS):      CA 134:38655
REFERENCE:              59
AUTHOR (AU):            Calabrese,D.; Bille,J.; Sanglard,D.
TITLE (TI):             A novel multidrug efflux transporter gene of the major
                        facilitator superfamily from Candida albicans (FLU1)
                        conferring resistance to fluconazole
JOURNAL (SO):           Microbiology (Reading, Engl.), 146 (PT 11), 2743-2754
                        (2000)
OTHER SOURCE (OS):      CA 135:1055
REFERENCE:              60
AUTHOR (AU):            Deising,H.B.; Werner,S.; Wernitz,M.
TITLE (TI):             The role of fungal appressoria in plant infection
JOURNAL (SO):           Microbes Infect., 2 (13), 1631-1641 (2000)
REFERENCE:              61 (bases 43783 to 45994)
AUTHOR (AU):            Smith,S.
TITLE (TI):             The world according to PARP
JOURNAL (SO):           Trends Biochem. Sci., 26 (3), 174-179 (2001)
OTHER SOURCE (OS):      CA 135:15779
REFERENCE:              62 (bases 131646 to 132375)
AUTHOR (AU):            Cronk,J.D.; Endrizzi,J.A.; Cronk,M.R.; O'neill,J.W.;
                        Zhang,K.Y.
TITLE (TI):             Crystal structure of E. coli beta-carbonic anhydrase,
                        an enzyme with an unusual pH-dependent activity
JOURNAL (SO):           Protein Sci., 10 (5), 911-922 (2001)
REFERENCE:              63 (bases 43783 to 45994)
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   AUTHOR (AU):          Ziegler,M.; Oei,S.L.
   TITLE (TI):           A cellular survival switch: poly(ADP-ribosyl)ation
                         stimulates DNA repair and silences transcription
   JOURNAL (SO):         Bioessays, 23 (6), 543-548 (2001)
REFERENCE:               64 (bases 43783 to 45994)
   AUTHOR (AU):          Herceg,Z.; Wang,Z.Q.
   TITLE (TI):           Functions of poly(ADP-ribose) polymerase (PARP) in DNA
                         repair, genomic integrity and cell death
   JOURNAL (SO):         Mutat. Res., 477 (1-2), 97-110 (2001)
   OTHER SOURCE (OS):    CA 136:145570
REFERENCE:               65 (bases 15614 to 17392)
   AUTHOR (AU):          Mundodi,S.R.; Watson,B.S.; Lopez-Meyer,M.; Paiva,N.L.
   TITLE (TI):           Functional expression and subcellular localization of
                         the Nectria haematococca Mak1 phytoalexin
                         detoxification enzyme in transgenic tobacco
   JOURNAL (SO):         Plant Mol. Biol., 46 (4), 421-432 (2001)
   OTHER SOURCE (OS):    CA 135:285870
REFERENCE:               66 (bases 1 to 163680)
   AUTHOR (AU):          Pel,H.J.; de Winde,J.H.; Archer,D.B.; Dyer,P.S.;
                         Hofmann,G.; Schaap,P.J.; Turner,G.; de Vries,R.P.;
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                         Heijden,R.T.; van der Kaaij,R.M.; Klis,F.M.;
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                         Lu,X.; van der Maarel,M.J.; Meulenberg,R.; Menke,H.;
                         Mortimer,M.A.; Nielsen,J.; Oliver,S.G.; Olsthoorn,M.;
                         Pal,K.; van Peij,N.N.; Ram,A.F.; Rinas,U.; Roubos,J.A.;
                         Sagt,C.M.; Schmoll,M.; Sun,J.; Ussery,D.; Varga,J.;
                         Vervecken,W.; van de Vondervoort,P.J.; Wedler,H.;
                         Wosten,H.A.; Zeng,A.P.; van Ooyen,A.J.; Visser,J.;
                         Stam,H.
   TITLE (TI):           Genome sequencing and analysis of the versatile cell
                         factory Aspergillus niger CBS 513.88
   JOURNAL (SO):         Nat. Biotechnol., 25 (2), 221-231 (2007)
   OTHER SOURCE (OS):    CA 146:310276
REFERENCE:               67 (bases 1 to 163680)
   AUTHOR (AU):          Pel,H.J.
   TITLE (TI):           Direct Submission
   JOURNAL (SO):         Submitted (01-MAY-2006) Pel H.J., DSM, 624-0295, P.O.
                         Box 1, 2600 MA Delft, THE NETHERLANDS
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                                         regulated by the phospholipid
                                         precursors inositol and choline
                                         and this regulation involves the
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                                         and Opi1p. Remark: alternate name
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in appressorium differentiation.
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exon         complement(9787..9927)    /locus-tag="An18g00990"
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mRNA         join(<10500..10749,       /locus-tag="An18g01000"
             10812..11041,
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CDS          join(10500..10749,        /locus-tag="An18g01000"
             10812..11041,
             11105..11479)

                                       /note="unnamed protein product;
                                       Similarity: the nucleotide
                                       sequence of the ORF shows strong
                                       similarity to the ESTs an-2192 and
                                       an-2204 of A. niger. Title: strong
                                       similarity to EST an-2192
                                       -Aspergillus niger"
                                       /codon-start=1
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                                       /translation="MYSYEKVNRDDDSDQGLLAE
                                       DSERVAPQPRVSRFPSWTNALLLL
                                       GLLFSLSLNVGWFVFQKGHNVPIQDLDPDAAMAK
                                       QRSPYTGLAWDTHKPYSHHSEYTS
                                       ENATHADEMWESLSMDPMVIAPTWEWAQSKGLSD
                                       SWAFPWDSNRRIYFIKVFHQLHCL
                                       KLMRHSYHELWSGQESSIPAPHIEHCLDSLRQDL
                                       MCKADDTPMPSLQLLNGGGEGQQM
                                       QCKDFDKLVAWSKAPERNACYKRLTDYKPIVHSI
                                       ERYAFCPEDSEHYPTMSKYFEEHG HYADPFSE"
exon         10500..10749              /locus-tag="An18g01000"
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intron       10750..10811              /locus-tag="An18g01000"
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exon         10812..11041              /locus-tag="An18g01000"
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intron       11042..11104              /locus-tag="An18g01000"
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exon         11105..11479              /locus-tag="An18g01000"
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gene         <11980..>13464            /locus-tag="An18g01010"
mRNA         join(<11980..12137,       /locus-tag="An18g01010"
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CDS          join(11980..12137,        /locus-tag="An18g01010"
             12198..13464)

                                       /inference="profile:COGS:COG0477"
                                       /note="unnamed protein product;
                                       Function: FLU1 of C. albicans
                                       facilitates resistance to
                                       fluconazole and cycloheximide in
                                       the fluconazole-hypersensitive S.
                                       cerevisiae strain YKKB-13 lacking
                                       the ABC (ATP-binding cassette)
                                       transporter gene PDR5. Function:
                                       FLU1 of C. albicans facilitates
                                       resistance to mycophenolic acid in
                                       C. albicans. Function: FLU1 of C.
                                       albicans is involved in the
                                       resistance to azol derivatives in
                                       C. albicans. Function: MDR1 of C.
```

albicans facilitates resistance to the anti-mitotic drug benomyl and to the dihydrofolate reductase inhibitor methotrexate. Similarity: N-terminus of the A. niger protein is app. 120 aa shorter than in FLU1 of C. albicans. Similarity: the predicted A. niger protein shows strong similarity to fluconazole resistance protein FLU1of C. albicans, which is a permease belonging to the major facilitator superfamily. Title: strong similarity to fluconazole resistance protein FLU1 - Candida albicans"
/citation=[59]
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gene	complement(<14029..>151 72)	/locus-tag="An18g01020"
mRNA	complement(join(<14029. .14318,14411..14845, 14917..>15172))	/locus-tag="An18g01020"
CDS	complement(join(14029.. 14318,14411..14845, 14917..15172))	/locus-tag="An18g01020"

/EC-number="1.13.11.4"
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/inference="similar to AA sequence:UniProtKB:AF173167.3"
/note="unnamed protein product; Complex: the estimated molecular mass of the purified gentisate 1, 2-dioxygenase of P. alcaligenes was 154 kDa, with a subunit mass of 39 kDa. its structure is

deduced to be a tetramer. Remark: gentisate 1,2-dioxygenase of P. alcaligenes exhibits typical saturation kinetics and has an apparent Km of 92 microM for gentisate. this enzyme has broad substrate specificities towards alkyl and halogenated gentisate analogs. Similarity: the predicted A. niger protein shows strong similarity to gentisate 1,2-dioxygenase of P. alcaligenes and conserved hypothetical proteins from other procaryotic species. Title: strong similarity to gentisate 1,2-dioxygenases xlnE - Pseudomonas alcaligenes"
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PNETAPAHRHTAFAMRYIIEGNGGFTAVHGKRIK
MQKGDVILTPTWNYHDHGKDGTGP
MIWLDGLDLPNFRHFPVHFVDHYDQPRYPAEDVD
SATSPIVFPWDKMKAELDKAPGTW
AVRRYLRADGSEGGSAERVDAGTSSLPRQETTSA
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TFCVPSWYKYRHIAAEGETVYLYRFDDKPMISAL
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		/number=2
exon	complement(14917..15172)	/locus-tag="An18g01020"
		/number=3
gene	<15614..>17392	/locus-tag="An18g01030"
mRNA	join(<15614..15661, 15723..16281, 16347..16503, 16584..16739, 16803..16942, 17034..>17392)	/locus-tag="An18g01030"
CDS	join(15614..15661, 15723..16281, 16347..16503, 16584..16739, 16803..16942, 17034..17392)	/locus-tag="An18g01030"
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                                              haematococca specifically
                                              hydroxylates the phytoalexins
                                              medicarpin and
                                              maackiain,converting them to less
                                              fungitoxic derivatives.
                                              Localization: heterologous
                                              expression of the Mak1 cDNA
                                              construct in plants indicated that
                                              Mak1 protein accumulates in the
                                              plant cytoplasm, associated with
                                              endoplasmic reticulum membranes.
                                              Similarity: the predicted A. niger
                                              protein shows strong similarity to
                                              Mak1 from the fungal pathogen N.
                                              haematococca. Mak1 belongs to the
                                              flavin-containing mono-oxygenases.
                                              best matches are with putative
                                              salicylate hydroxylases of several
                                              procaryotic species. Title: strong
                                              similarity to maackiain
                                              detoxification protein 1 MAK1 -
                                              Nectria haematococca endoplasmatic
                                              reticulum"
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                                              GLQSYLEPYVTAPESISFRRWQNGKVIGLTKLIP
                                              NFVNNFKAPYYVIHRADFHSALCQ
                                              KALDVGVEIELGAKVVDYDPIVGSITLADGTKHS
                                              ADLIVAADGIKSVARNVVLQGDEM
                                              RFQGPGFAAYRAVVDVGKMRRDPDLSWILEKPAL
                                              NIWIGDSRHVMTYTIGAGKAFNMV
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                                              IIGMVEKTVKWPLLTGTLLQNWTV
                                              GKLVILGDAAHAMVPYMSQGAAMAVEDGIALSRS
                                              LSHMTSRDQLQKALSIFQEVRKKR
                                              AGHMQEASLLNGKLWHFPDGSLQQARDEAMAPEV
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gene	<17766..>20491	/locus-tag="An18g01040"
mRNA	join(<17766..17864,	/locus-tag="An18g01040"
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	18398..19163,	
	19373..19935,	
	20037..20252,	
	20325..>20491)	
CDS	join(17766..17864,	/locus-tag="An18g01040"
	17939..18039,	
	18108..18343,	
	18398..19163,	
	19373..19935,	
	20037..20252,	
	20325..20491)	

/inference="profile:PFAM:PF00172"
/inference="similar to AA
sequence:UniProtKB:ENU56097.1"
/note="unnamed protein product;
Phenotype: facB recessive loss of
function mutants in A. nidulans
are deficient in acetate induction
of acetyl-CoA synthase, isocitrate
lyase, malate
synthase,acetamidase, and
NADP-isocitrate dehydrogenase.
Similarity: the predicted A. niger
protein shows similarity to
acetate regulatory DNA binding
protein FacB (facB) from A.
nidulans, which belongs to the
GAL4-type zinc cluster
transcriptional activators. Title:
similarity to acetate regulatory
DNA binding protein facB -
Aspergillus nidulans"
/citation=[37]
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/protein-id="CAK47181.1"
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DAPRKENPLSNQSERFSDFAGTEDTIDAMGAVAF
ADEEDCGFFGPSSNIAFLRHLSCA
VAHSASAQKEITSPPLDRVAYDGGFVSATRPSSP
SHDQRPESLEGEKFDKFALPPPEE
SLALIHRYFADTGLLFPYIHPPTFFETYAELKDN
SKRVRRTWLGLLNIILAMAKLTAV
SGTTSAETGISESAIYYHRALSLCKGEILRGTTL
EVGRYSIYAPVRARVPVYLRATKI
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QLGLHSKGASRAFTPLEQEVRKRT

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                                          IERSEVGDEGHHKLYPLKFRIILT
                                          LRYFHVQILLHRPILVKFLDATGPSGLEADEVKL
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                                          ELVSTTGWQKDLLGAWWYSLYYTFNAALVIIGAM
                                          WVQRNRDTSEDPVDNGGNNNNMDI
                                          YLSRAVLTLQNLNVGNRMVDRCKYYLDQLITLLG
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mRNA	complement(join(<20773. .21444,21501..21638, 21710..22119, 22180..22303, 22370..>22555))	/locus-tag="An18g01050"
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```
```

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                              Cofactor:
                              lignostilbene-alpha,beta-dioxygena
                              se isozymes (LSD-I, II, and III)
                              of P. paucimobilis require iron as
                              a cofactor. Complex: LSD-I, II,
                              and III consist of alpha
                              alpha,alpha beta, and beta beta
                              subunits, respectively. they show
                              different specificities for
                              several substrates that are
                              stilbene and styrene derivatives.
                              Function: LSD of P. paucimobilis
                              catalyses the oxidative cleavage
                              of the interphenyl double bond in
                              the synthetic substrate and
                              lignin-derived stilbenes. it is
                              responsible for the degradation of
                              a diarylpropane-type structure in
                              lignin. Similarity: the predicted
                              A. niger protein shows strong
                              similarity to subunit lsdB of
                              lignostilbene-alpha,beta-dioxygena
                              se isozyme LSD-III of P.
                              paucimobilis and related
                              dioxygenases from several plant
                              species. Title: strong similarity
                              to subunit lsdB of
                              lignostilbene-alpha,beta-dioxygena
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                              IAQLTLFLWSIEGKYRNKFTDAVEFKVRSTANTN
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                              EVVWLVAPVVAMIHDFAVTDNWVIFPIIPQLCDI
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                              YRIDDRYATKPHRHVFFDMMDPSL
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exon              complement(21501..21638 /locus-tag="An18g01050"
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                                            /note="unnamed protein product;
                                            Catalytic activity:
                                            5-carboxymethyl-2-hydroxymuconate
                                            delta-isomerase from E. coli
                                            catalyses the reaction
                                            5-carboxymethyl-2-hydroxymuconate
                                            = 5-carboxy-2-oxohept-3-enedioate.
                                            Pathway:
                                            5-carboxymethyl-2-hydroxymuconate
                                            delta-isomerase from E. coli is
                                            involved in tyrosine and
                                            phenylalanine metabolism.
                                            Similarity: the predicted A. niger
                                            protein shows strong similarity to
                                            5-carboxymethyl-2-hydroxymuconate
                                            delta-isomerase from E. coli and
                                            many putative
                                            2-hydroxyhepta-2,4-diene-1,
                                            7-dioate isomerases from several
                                            procaryotic and eucaryotic
                                            organisms. Title: strong
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              27423..27426)
                                       /inference="profile:COGS:COG0477"
                                       /note="unnamed protein product;
                                       Function: FLU1 of C. albicans
                                       facilitates resistance to
                                       fluconazole and cycloheximide in
                                       the fluconazole-hypersensitive S.
                                       cerevisiae strain YKKB-13 lacking
                                       the ABC (ATP-binding cassette)
                                       transporter gene PDR5. Function:
                                       FLU1 of C. albicans facilitates
                                       resistance to mycophenolic acid in
                                       C. albicans. Function: FLU1 of C.
                                       albicans is involved in the
                                       resistance to azol derivatives in
                                       C. albicans. Function: MDR1 of C.
                                       albicans facilitates resistance to
                                       the anti-mitotic drug benomyl and
                                       to the dihydrofolate reductase
                                       inhibitor methotrexate.
                                       Similarity: N-terminus of the A.
                                       niger protein is app. 120 aa
                                       shorter than in FLU1 of C.
                                       albicans. Similarity: the
                                       predicted A. niger protein shows
                                       strong similarity to fluconazole
                                       resistance protein FLU1of C.
                                       albicans, which is a permease
                                       belonging to the major facilitator
                                       superfamily. Title: similarity to
                                       fluconazole resistance protein
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                                    FLU1 - Candida albicans"
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                                    MGGAGLSVAVPVLMQQLQRSQAEVTQLLTLNFLF
                                    LGIGNIFWVPLAVKFGKRASIISS
                                    MLLQAGALVWCAVATGYDSLLGARCVLGFAAAAG
                                    ESIVPEIVADIFFVHERATMMAIY
                                    VVLISGGSAVGPLIGGFMVEYASGTWRSYMWLCF
                                    ALASFNIVLLVFLFPESTFKRPEP
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exon              25166..25301       /locus-tag="An18g01070"
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intron            25302..25563       /locus-tag="An18g01070"
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exon              25564..25745       /locus-tag="An18g01070"
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intron            25746..25811       /locus-tag="An18g01070"
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intron            26647..26721       /locus-tag="An18g01070"
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exon              26722..27303       /locus-tag="An18g01070"
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intron            27304..27422       /locus-tag="An18g01070"
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exon              27423..27426       /locus-tag="An18g01070"
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gene              complement(<27797..>286  /locus-tag="An18g01080"
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mRNA              complement(join(<27797.  /locus-tag="An18g01080"
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                  28450..28550,
                  28602..>28667))
CDS               complement(join(27797..  /locus-tag="An18g01080"
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                  28450..28550,
                  28602..28667))
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                                           /db-xref="GI:134084152"
                                           /translation="MGPRKAFLNGYIVVVRRIQP
                                           WRALAAQAVPLIHTSNADSSPATG
                                           FYSLRFVVSHPHPPTVPANHTVSGTNTSFDRHVI
                                           LVSNNSQWIINPWSIGRTLSWPGP
                                           VKSLEAGRYGHLRKHNPAAYEELNFASSNKHCCC
                                           VMLRAYYYPRVQEEYLLRLFLYRC
                                           LKDTASFATVRKKDQSLNVHESLQSTYPGGIFRV
                                           AAKADFPAEGSKSFRTQTMCWALL LKYGVF"
sig-peptide       complement(join(28506.. /locus-tag="An18g01080"
                  28550,28602..28667))
                                           /inference="protein
                                           motif:SignalP:2.0"
mat-peptide       complement(join(27800.. /locus-tag="An18g01080"
                  28220,28259..28342,
                  28450..28505))
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exon              complement(27797..28220 /locus-tag="An18g01080"
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intron            complement(28221..28258 /locus-tag="An18g01080"
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exon              complement(28259..28342 /locus-tag="An18g01080"
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                                           /number=2
intron            complement(28343..28449 /locus-tag="An18g01080"
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exon              complement(28450..28550 /locus-tag="An18g01080"
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intron            complement(28551..28601 /locus-tag="An18g01080"
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                                           /number=3
exon              complement(28602..28667 /locus-tag="An18g01080"
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                                           /number=4
gene              <28874..>30837          /locus-tag="An18g01090"
mRNA              join(<28874..29683,     /locus-tag="An18g01090"
                  29736..29875,
                  29925..>30837)
CDS               join(28874..29683,      /locus-tag="An18g01090"
                  29736..29875,
                  29925..30837)
                                           /EC-number="3.1.1.5"
                                           /inference="profile:PFAM:PF01735"
                                           /note="unnamed protein product;
                                           Catalytic activity:
                                           lysophospholipase catalyses the
                                           reaction 2-lysophosphatidylcholine
                                           + H(2)O = glycerophosphocholine +
                                           a fatty acid anion. Pathway:
                                           lysophospholipase is involved in
                                           phospholipid degradation.
                                           Similarity: the predicted A. niger
```

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                                    protein shows strong similarity to
                                    the protein sequences
                                    lysophospholipase (sequence 5 and
                                    sequence 7) of patents
                                    WO0127251-A/5 and WO0127251-A/7
                                    from A. oryzae (AC# AX112082 and
                                    AC# AX112084) and to other fungal
                                    lysophospholipases. Title: strong
                                    similarity to lysophospholipase
                                    from patent WO0127251-A -
                                    Aspergillus oryzae
                                    extracellular/secretion proteins"
                                    /citation=[14]
                                    /codon-start=1
                                    /protein-id="CAK47186.1"
                                    /db-xref="GI:134084153"
                                    /translation="MLSLLISAAAATLASALELP
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                                    RDEAQWVEGRKNVILGSLDAYLKRLNLDDFDTDE
                                    YISRLNNTSQTPIMGMAISGGGFG
                                    SAYTGTGLIRALDDRLPAANEQRTGGLLQSMTYL
                                    SGLSGGSWPAVSFPSYNFPTADEI
                                    VDYWKPEIDRFFTVTNTSAEAATGKAIFEQIATK
                                    YLAGFEVALSDYLGRGFAYEFIPG
                                    QSGGLNTTFSGIRNLSNFINHQMPMPIIHLASVE
                                    PEDAEYYDLLVPSSNGTIFDLTPF
                                    EFGAWDGDVHAFTPTEWLGNQLSNGIPVNQSKCW
                                    KGFDRSSLVIGTSADAFNFWYLES
                                    VSNGTLGQFAKRSTTHESSLTKRLSQPANLNALV
                                    DAFQETFDLNLTQISYSKFPNPFT
                                    NLSLSTGNTHKSSTLNLVDGSETGQTIPLWGQIQ
                                    PARNVDFIIAWDDSQDADPYSWNN
                                    GTNLYNTYLAANATGLPFPIIPPSRTMMNLNYTL
                                    HPQFFGCDANLTTTGDDRAPIVLY
                                    MANAPYSAYTNFSFWQTETSRQQMGEIFVNSFDI
                                    VTQANGSWDGEWAECMGCAAVERS
                                    LARVGMERTRQCQRCFERYCWDGTLDERDPGVLD
                                    PTLVLDPGVKFGLWNATNPY"
     sig-peptide    28874..28921        /locus-tag="An18g01090"
                                        /inference="protein
                                    motif:SignalP:2.0"
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                    29736..29875,
                    29925..30834)
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     intron         29684..29735        /locus-tag="An18g01090"
                                        /number=1
     exon           29736..29875        /locus-tag="An18g01090"
                                        /number=2
     intron         29876..29924        /locus-tag="An18g01090"
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     exon           29925..30837        /locus-tag="An18g01090"
                                        /number=3
     gene           complement(<30960..>322 /locus-tag="An18g01100"
                    18)
     mRNA           complement(join(<30960. /locus-tag="An18g01100"
                    .31045,31081..31220,
                    31273..31630,
                    31702..>32218))
     CDS            complement(join(30960.. /locus-tag="An18g01100"
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                     31045,31081..31220,
                     31273..31630,
                     31702..32218))
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                                        /inference="profile:PFAM:PF00107"
                                        /note="unnamed protein product;
                                        Remark: the patent does not
                                        provide further information about
                                        the function of the protein.
                                        Similarity: the predicted A. niger
                                        protein shows strong similarity to
                                        the protein sequence alcohol
                                        dehydrogenase (sequence 19) of
                                        patent EP0845532-A/19 from an
                                        unclassified organism (AC# A92108)
                                        and to other zinc-containing
                                        dehydrogenases. Title: strong
                                        similarity to alcohol
                                        dehydrogenase from patent
                                        EP0845532-A - Unclassified
                                        organism cytoplasm"
                                        /codon-start=1
                                        /protein-id="CAK47187.1"
                                        /db-xref="GI:134084154"
                                        /translation="MSHAQITHRRAVRRTDDYTP
                                        HTPKVNIVTEPLPLPLSPTAVLIR
                                        VHAVALNYRDANIANGGNPWPVLPHGILGNDAAG
                                        EVIAVGEKVKTLAVGDRAAPITDT
                                        EQITERATKRSWLAADEDGVMADYIVYDESVLCK
                                        LPAYLDWVQASMIPCAGVTAWSAL
                                        KGMRIGQTVLVQGTGGVSMFALKLALAAGLRVVL
                                        TSSSDAKLQAIKEKYAGSAILTVN
                                        YKNTPEWDEEVLKLTGGVGVDLVVENGGTGSLVK
                                        SMRCTRRGGVVSQVGYLGKQDPSE
                                        LSELVPTLIDRRINLRGINAGSKLDMEDFCEALS
                                        ASQTLLDDLIDKVFPFEQAEEAVE
                                        YVWQEKDIGSERKIQNSFYHLGSYVGTWSSAS"
     exon            complement(30960..31045 /locus-tag="An18g01100"
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     exon            complement(31081..31220 /locus-tag="An18g01100"
                     )
                                        /number=2
     intron          complement(31221..31272 /locus-tag="An18g01100"
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                                        /number=2
     exon            complement(31273..31630 /locus-tag="An18g01100"
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     intron          complement(31631..31701 /locus-tag="An18g01100"
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                                        /number=3
     exon            complement(31702..32218 /locus-tag="An18g01100"
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                                        /number=4
     gene            <32976..>33236         /locus-tag="An18g01110"
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exon	32976..33236	/locus-tag="An18g01110" /number=1
gene	complement(<33419..>354 77)	/locus-tag="An18g01120"
mRNA	complement(join(<33419. .33465,33522..34023, 34080..34956, 35015..35044, 35095..>35477))	/locus-tag="An18g01120"
CDS	complement(join(33419.. 33465,33522..34023, 34080..34956, 35015..35044, 35095..35477))	/locus-tag="An18g01120"
		/EC-number="1.-.-.-" /inference="profile:COGS:COG2303" /inference="profile:PFAM:PF00732" /inference="profile:PFAM:PF05199" /note="unnamed protein product; Catalytic activity: versicolorin B synthase from A. parasiticus catalyses the side chain cyclization of racemic versiconal hemiacetal to the bisfuran ring system of(-)-versicolorin B. Pathway: versicolorin B synthase from A. parasiticus is involved in the aflatoxin biosynthetic pathway. Remark: a splice site was detected upstream of the START codon. Remark: aflatoxins comprise a group of polyketide-derived carcinogenic mycotoxins. Remark: the genes encoding the aflatoxin biosynthetic enzymes in A. parasiticus are clustered. Remark: versicolorin B synthase from A. parasiticus possesses an amino-terminal sequence homologous to the ADP-binding region of other flavoenzymes, but does not require flavin or nicotinamide cofactors for its cyclase activity. Similarity: the predicted A. niger protein shows strong similarity to versicolorin B synthase from A. parasiticus and other oxidoreductases. Title: strong similarity to versicolorin B synthase vbs - Aspergillus parasiticus" /citation=[30] /codon-start=1

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                                   /translation="MIRHVLLSLALQCMVTGTIA
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                                   VGGGTAGNTIATRLAQKNYKVAVIEAGGSYELES
                                   VAEVPAADVLPVGSDPETAAAHDW
                                   GFVAENVPGANGRSIHYARGKCWGGSSAMNFMIY
                                   QRPTIESMEQWATAVNDSSYTFDQ
                                   TLPFYKNSVKFTPPNTQIRAKNATAGYDPSAYES
                                   TGGPLKVSYANYAMPFSTWMDLGM
                                   KAIGINETQDFNLGSLMGGQYCASTIDPNGEVRS
                                   SSEESFLANKPSTLTTYANTLAKK
                                   IIFNNQKQATGVQVKGSAGNIYTIKANREVIVSA
                                   GAFQSPQLLMVSGVGPQDQLEEHG
                                   IQVVANRPGVGQNMWDHPFFAPSYRVNVQTFTAI
                                   ANDFLGIVGQFINMVGFGNGPLTN
                                   PISDYLAWEKIPAALRSAFSSQTTKQLATFPSDW
                                   PEAEYISGAGYMGNVSNLLINQPE
                                   DGYQYASMLAVLITPTSRGNITLRSADTDDLPVI
                                   NPNWLATQSDQEVAIAMFKRVRAA
                                   FQSKAMAPVIIGNEYNPGLEVQSDEQILQWIKDN
                                   VMTLWHAACTCKMGTSDDEMAVVD
                                   SQARVYGVQGVRVVDASAFPFLPPGHPQSTVYML
                                   AEKIANEIINGA"
sig-peptide        complement(35418..35477  /locus-tag="An18g01120"
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mat-peptide        complement(join(33422..  /locus-tag="An18g01120"
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                   34080..34956,
                   35015..35044,
                   35095..35417))
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exon               complement(33419..33465  /locus-tag="An18g01120"
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                                            /number=1
intron             complement(33466..33521  /locus-tag="An18g01120"
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exon               complement(33522..34023  /locus-tag="An18g01120"
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                                            /number=2
intron             complement(34024..34079  /locus-tag="An18g01120"
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intron             complement(34957..35014  /locus-tag="An18g01120"
                   )
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exon               complement(35015..35044  /locus-tag="An18g01120"
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intron             complement(35045..35094  /locus-tag="An18g01120"
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exon               complement(35095..35477  /locus-tag="An18g01120"
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gene               <37406..>38455           /locus-tag="An18g01130"
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                                        /note="unnamed protein product;
                                        Remark: the patent does not
                                        provide further information about
                                        the function of the protein.
                                        Similarity: the predicted A. niger
                                        protein shows similarity to the
                                        protein fragment (SEQ ID NO:
                                        51484) of patent EP1033405-A2 from
                                        A. thaliana (AC# AAG41385) and to
                                        putative sterol desaturase family
                                        proteins. Title: similarity to
                                        protein fragment SEQ ID NO:51484
                                        from patent EP1033405-A2 -
                                        Arabidopsis thaliana"
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                                        /protein-id="CAK47190.1"
                                        /db-xref="GI:134084157"
                                        /translation="MSGTHPNPKDSMKSTWRRLD
                                        RAEWTIYHWFYEILGVHPEHLDKE
                                        VPVHQKTEKIPYMRTWSQHVWILYHAFIPLAVHH
                                        VYVSYTGQNFTPVGAFFFYSIAFK
                                        LIAIHQLQVMRRMGHVLGFLDGDQHGRDGVPDVG
                                        VAKVVRSLISTSTFRPIMTVFLSY
                                        RVSQAPAQMSWGWLPLEIGLYGIILDFWFYWYHR
                                        LMHDVGSLWKYHRTHHLTKHPNPL
                                        LTLYADTEQEFFDIAGIPLMTYFSMRLMGMPMGF
                                        YEWWICHQYVVFTELAGHSGLRMH
                                        ASPPSTLDWLLRLIGAELVIEDHDLHHRKGWKKS
                                        HNYGKQTRLWDKIFGTCHERIESR
                                        EGNVDYDNTVRMPIF"
exon            37406..38455            /locus-tag="An18g01130"
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gene            <38805..>39836          /locus-tag="An18g01140"
mRNA            <38805..>39836          /locus-tag="An18g01140"
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                                        /inference="profile:PFAM:PF02558"
                                        /note="unnamed protein product;
                                        Title: similarity to ketopantoate
                                        reductase -Salmonella typhimurium
                                        cytoplasm"
                                        /citation=[23]
                                        /citation=[42]
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                                        SLRSLPAPPPITILLHRESAYQDF
                                        LSGGSKLRLQIGEDGPTQETTGYDAELLQGESPI
                                        QHLIVAVKASATIPALRSIQHRLG
                                        RHSVICLFQNGLGQIEELNERLFTDPLTRPTYMF
                                        GIMRHGVYIKAPFEAVLAGLTGSC
                                        ALGIVNNDQQASSLSASSTASAQSRFLINRLVEA
                                        PIVRSSELPWMELHQAQLLKLATN
                                        CVVNPLTALLDVRNGSLLANSELQEMRRQLLQEI
                                        SLVFRRLPEFQGLPDVEEQFSVAR
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                                        NGWIVRRGQQLGLDCPTNRCLTQL
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mat-peptide     38877..39833              /locus-tag="An18g01140"
                                          /product="unnamed"
exon            38805..39836              /locus-tag="An18g01140"
                                          /number=1
gene            <40728..>42671            /locus-tag="An18g01150"
mRNA            join(<40728..41152,       /locus-tag="An18g01150"
                41226..42344,
                42401..>42671)
CDS             join(40728..41152,        /locus-tag="An18g01150"
                41226..42344,
                42401..42671)

                                          /inference="profile:COGS:COG0477"
                                          /inference="similar to AA
                                          sequence:UniProtKB:AF188621.1"
                                          /note="unnamed protein product;
                                          Function: FLU1 of C. albicans
                                          facilitates resistance to
                                          fluconazole and cycloheximide in
                                          the fluconazole-hypersensitive S.
                                          cerevisiae strain YKKB-13 lacking
                                          the ABC (ATP-binding cassette)
                                          transporter gene PDR5. Function:
                                          FLU1 of C. albicans facilitates
                                          resistance to mycophenolic acid in
                                          C. albicans. Function: FLU1 of C.
                                          albicans is involved in the
                                          resistance to azol derivatives in
                                          C. albicans. Function: MDR1 of C.
                                          albicans facilitates resistance to
                                          the anti-mitotic drug benomyl and
                                          to the dihydrofolate reductase
                                          inhibitor methotrexate.
                                          Similarity: the predicted A. niger
                                          protein shows strong similarity to
                                          fluconazole resistance protein
                                          FLU1of C. albicans, which is a
                                          permease belonging to the major
                                          facilitator superfamily. Title:
                                          strong similarity to fluconazole
                                          resistance protein FLU1 - Candida
                                          albicans"
                                          /citation=[59]
                                          /codon-start=1
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                                          /db-xref="GI:134084159"
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                                          GASKEEGLERPSSSGTTGSTGYSS
                                          SLEYNPQLHTLHSRNTELDLERHRTATSHALSRI
                                          ETQRLQHQLTVGESVKSRASRTPL
                                          PRMGANKDYPPPLPDREDYVVEFDGPEDPLYPQN
                                          WELGTKIYISAILAFTSICSTFDS
                                          AIFSSSTTNVARVFGVGIEVATLSSSLYICGYAS
                                          GPLVWAPLSELKGRKPPIVVAMLG
                                          FGIFNTAVAVAKDLQTIMICRFFCGVFGSCPLAV
                                          VAAVFSDIYNNRTRGVAIAMFSST
                                          VFLGPLLAPFIGGFINTSYLGWRWTAYIPAFMGY
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                                          ELRRRTKNWGIHAKQEEIEVDLRELLVNNFSRPL
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                                        RLLFGEPLILAVTIYLSFIYGLLY
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                                        AASYIIFASRGYNKKLEANGGIPV
                                        PEWRLPPVIIGGALFAGGLFWFGWTGFTKSIHWI
                                        VPTLSGLFTGLGLLIIFIQLFNYL
                                        IDTYLMFAASAIAANTFCRSLVAASFPLFSRQMF
                                        NNMGIQWAATLLGCVASILVPIPV
                                        AFYFYGKNLRKRSKFAPFYDKVAESHAEDPVENG
                                        VAEH"
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                                        /number=1
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     exon           41226..42344        /locus-tag="An18g01150"
                                        /number=2
     intron         42345..42400        /locus-tag="An18g01150"
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     exon           42401..42671        /locus-tag="An18g01150"
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     gene           42950..43033        /gene="tRNA-His (GTG)"
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     tRNA           42950..43033        /gene="tRNA-His (GTG)"
                                        /locus-tag="An18e01160"
                                        /product="tRNA-His"
                                        /inference="profile:tRNAscan:1.4"
                                        /note="codon recognized: CAC"
     gene           <43783..>45994      /locus-tag="An18g01170"
     mRNA           join(<43783..43852,  /locus-tag="An18g01170"
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                    44395..45240,
                    45294..45376,
                    45425..>45994)
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                    44395..45240,
                    45294..45376,
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                                        /inference="profile:PFAM:PF00644"
                                        /inference="profile:PFAM:PF02877"
                                        /note="unnamed protein product;
                                        Catalytic activity: the NAP
                                        protein of Z. mays catalyses the
                                        reaction NAD(+) +
                                        {ADP-D-ribosyl}(N)-acceptor <=>
                                        nicotinamide +
                                        {ADP-D-ribosyl}(N+1)-acceptor.
                                        Function: the NAP protein of Z.
                                        mays is involved in programmed
                                        cell death or apoptosis.
                                        Localization: the NAP protein of
                                        Z. mays is a nuclear enzyme.
                                        Remark: the ADP-D-ribosyl group of
                                        NAD(+) is transferred to an
                                        acceptor carboxyl group on a
                                        histone or the enzyme itself, and
                                        further ADP-ribosyl groups are
                                        transferred to the 2'-position of
                                        the terminal adenosine moiety,
                                        building up a polymer with an
```

average chain length of 20-30
units. Remark: the NAP
polynucleotide sequences can be
used for modulation of programmed
cell death in eukaryotic cells.
the method is used, specifically
in plants, to induce, or protect
against, programmed cell
death,depending on the extent to
which PARP activity is reduced.
reducing expression of endogenous
NAP class PARP only is also used
to modulate programmed cell death,
to increase growth rate and to
produce plant cells that are more
tolerant of stress (cold, chemical
treatments, pathogens,pests,
drought, heat, etc. , or during
transformation). particular
applications are generation of
plants that are resistant to fungi
or nematodes; are male or female
sterile ; or have better
seed-shatter properties. the
methods are also used to improve
growth of transformed plant cells
(and derived calli or complete
plants). Similarity: the predicted
A. niger protein shows st
rong similarity to the protein
sequence poly(ADP-ribose)
polymerase NAP protein of patent
WO200004173-A1 from Z. mays (AC#
AAY68834) and from many other
eucaryotic organisms. Title:
strong similarity to
poly(ADP-ribose) polymerase NAP
protein from patent WO200004173-A1
- Zea mays nucleus"
/citation=[61]
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DDEPESPKKRTLEQALGINEDGTTKKLKDAQTVG
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TGLIWDATLNQTSATNNNNKFYRIQLLHRNNEFR
TWTHWGRVGEHGQHALLGGGGLDE
AEYEFKKKFKDKSGLTWENRLDPPKKGKYTFIEK
NYEEDTEDEDEDEDKVVAKKPTKP
KAEEVKCTLSAPVQDLVSFIFNKDFFQSTMASMS
YDAQKLPLGKLSKRTLQNGFQALK
DLSELIANPALASTKYDTSFTAAVEHLSNLYFTV
IPHAFGRNRPPVLNNDNLLKREIE
LLEALTDMEVANSIMKDARNTDTVHPLDRQFQGL
NMQEMTPLEHTSTEFIELANYLNQ
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mRNA            join(<46879..48454,      /locus-tag="An18g01180"
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                48518..48537)
                                         /EC-number="3.5.1.11"
                                         /note="unnamed protein product;
                                         Function: penicillin V
                                         amidohydrolase (PVA) from F.
                                         oxysporum is used for the
                                         enzymatic hydrolysis of penicillin
                                         V (phenoxy-methylpenicillin) to
                                         6-aminopenicillanic acid (6-APA).
                                         6-APA is the active beta-lactam
                                         nucleus used in the manufacture of
                                         semi-synthetic penicillins.
                                         Similarity: the predicted A. niger
                                         protein shows strong similarity to
                                         the protein sequence penicillin V
                                         amidohydrolase (PVA) of patent
                                         US5516679-A from F. oxysporum (AC#
                                         AAW00291). Title: strong
                                         similarity to penicillin V
                                         amidohydrolase PVA from patent
                                         US5516679-A - Fusarium oxysporum
                                         extracellular/secretion proteins"
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                                          CPFKPETLVGHTVTCPEMGSDSPVTITAQHATLV
                                          KQILQGPDLQDHPDLWTGLPPGAS
                                          FRGTANTQVINGSIVRPVPFFPIIGWIKNFVYRD
                                          PDYNVFDMTFDDFNTAYRLTLDGY
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CDS             join(49850..49888,        /locus-tag="An18g01200"
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                                          /inference="profile:PFAM:PF00067"
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                                          sequence:UniProtKB:AFU81806.1"
                                          /note="unnamed protein product;
                                          Function: ord1 of A. flavus
                                          converts O-methylsterigmatocystin
                                          to aflatoxin B1. Pathway: ord1 of
                                          A. flavus catalyzes the last step
                                          of the aflatoxin biosynthetic
                                          pathway. Remark: aflatoxins
                                          comprise a group of
                                          polyketide-derived carcinogenic
                                          mycotoxins. Similarity: the
                                          predicted A. niger protein shows
```

strong similarity to
O-methylsterigmatocystin
(OMST)-oxidoreductase (ord1) from
A. flavus, which belongs to the
CYP64 family of cytochrome
P450-type monooxygenases. Title:
strong similarity to
O-methylsterigmatocystin
oxidoreductase ord1 - Aspergillus
flavus"
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FRATRKNLHREIGSNVSVARFNEI
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PHDQDPLVDLADKAMMDFSMAMLP
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TAFSDIPYAFVKEQMRTGRFVPSF
LSNLLESSDLEPGSEEENTVKWSAGSLYAGGADT
TVSSIASFFLAMALFPEVQRKAQQ
ELDTVIGTDRLPQYADREQLPYINALVKETFRWH
PVVPMSLTHTSTADDVCEGYFIPK
GSSVLANIWAFTHDPAAYHDPMTFKPERFLSPKP
ERDPHFLVFGFGRRVCPGRTLADV
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exon	50883..51127	/locus-tag="An18g01200" /number=6
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                                    /note="unnamed protein product;
                                    Function: SRPK2 from M. musculus
                                    phosphorylates SF2/ASF, a member
                                    of SR splicing factors. Remark:
                                    overexpression of murine SRPK2
                                    causes disassembly of
                                    cotransfected SF2/ASF and
                                    endogenous SC35. SRPK family
                                    members may regulate the
                                    disassembly of the SR proteins in
                                    a tissue-specific manner.
                                    Similarity: the predicted A. niger
                                    protein shows similarity to SRPK2
                                    from M. musculus and strong
                                    similarity to putative
                                    serine/threonine protein kinases
                                    from several eucaryotic organisms.
                                    Title: similarity to
                                    SR-protein-specific kinase SRPK2 -
                                    Mus musculus nucleus"
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intron          complement(52360..52410 /locus-tag="An18g01210"
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exon            complement(52411..52573 /locus-tag="An18g01210"
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                                              /inference="similar to AA
                                              sequence:PIR:S64826"
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                                              Function: in S. cerevisiae,
                                              mutants (dal5) that lack
                                              allantoate transport have been
                                              isolated. these strains also
                                              exhibit a 60% loss of allantoin
                                              transport capability. Regulation:
                                              in S. cerevisiae Dal5 appears to
                                              be sensitive to nitrogen
                                              catabolite repression, feedback
                                              inhibition, and trans-inhibition.
                                              Regulation: in S. cerevisiae
                                              allantoate uptake is constitutive.
                                              Similarity: the predicted A. niger
                                              protein shows strong similarity to
                                              allantoate permease gene (DAL5)
                                              from S. cerevisiae, which belongs
                                              to the major facilitator
                                              superfamily. Title: strong
                                              similarity to allantoate permease
                                              Dal5 - Saccharomyces cerevisiae"
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                                              /citation=[9]
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                                          TVLIGVLTLLFIPDTPMKAKWLSEEEKVALLQHV
                                          SVNQTGVWSSAINLKQIWEGVLDI
                                          QLWLLVLITILISVSSGVVTTYSATLIAGFGYSG
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                                          IRRTSHRWAWNAFCTIPGIIGGGLLSFLPKSNKA
                                          GVLIGIYLVNAIVATLPILYQWTM
                                          ANCAGHTKRAFSSALIAGSFSVGNIIGPQTFQAR
                                          DAPEYRPAKIAVLATQAAAAVMSV
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mRNA	join(<56384..56645, 56694..56761, 56818..57009, 57069..57368, 57430..57711, 57897..58158, 58326..>58444)	/locus-tag="An18g01230"
CDS	join(56384..56645, 56694..56761, 56818..57009, 57069..57368, 57430..57711, 57897..58158, 58326..58444)	/locus-tag="An18g01230"
		/note="unnamed protein product; Function: M. grisea Pth11 is a pathogenicity gene. Function: M. grisea Pth11p likely is involved in host surface recognition. Function: M. grisea pth11 mutants of strain 4091-5-8 are nonpathogenic due to a defect in appressorium differentiation. Localization: in M. grisea, a Pth11-green fluorescent protein

fusion localised to the cell
membrane and vacuoles. Similarity:
similarity of the predicted A.
niger protein and M. grisea Pth11
is limited to the N-terminal half
of the protein sequences. Title:
similarity to integral membrane
protein PTH11 - Magnaporthe grisea
plasma membrane"
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ADLPDYTKLNYAGRPFYQLGIAGFKASLCLNYLR
LISGTSKNFYRILIWAVIAVSTLG
HLAGTLVLIFDCQPVERAWNPNISGSCLPAGPTF
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LNIKTAQKAGVVCLFLLGLFTTICSILRLTQIHR
VAYGDGNSTMLVLWGTIEFNVGNI
VTCVPFLAPLLKGAVRDFRSYSGRKGYDSRSYAL
QTWSKDPRSQLRSTTSAAPQPKRT
PSEELILESGGVDEGGIHMTVELRVSLEKRPTTE
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DTSQWSRAEQARPTVPDGIFPAIKPSSIQEESCA
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intron	57369..57429	/locus-tag="An18g01230" /number=4
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gene	<59070..>60560	/locus-tag="An18g01240"
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                                                /note="unnamed protein product;
                                                Catalytic activity: NahW of P.
                                                stutzeri catalyzes the conversion
                                                salicylate + NADH + O(2) <=>
                                                catechol + NAD(+) + H(2)O + CO(2).
                                                Pathway: NahW of P. stutzeri is
                                                involved in the metabolization of
                                                naphtalene and salicylates (lower
                                                naphtalene degradation pathway).
                                                Similarity: the predicted A. niger
                                                protein shows similarity to
                                                salicylate hydroxylase (nahW) of
                                                P. stutzeri,which belongs to the
                                                NADH-dependent monooxygenase
                                                superfamily. Title: similarity to
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                                                -Pseudomonas stutzeri"
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                                                AGAAEIDPFIFQGSHPESNVFLFF
                                                SILDTPNNFVESSKDKYECQIILSWADSKDIAVP
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                                                VHRLSEDTEARSIRIADWMFRPLQNRSHPRVVLM
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mat-peptide             join(59127..59441,      /locus-tag="An18g01240"
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gene            complement(<60793..>611  /locus-tag="An18g01250"
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mRNA            complement(join(<60793.  /locus-tag="An18g01250"
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intron	complement(65229..65471)	/locus-tag="An18g01280"
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		/number=4
gene	<66055..>67388	/locus-tag="An18g01290"
mRNA	join(<66055..66654, 66723..>67388)	/locus-tag="An18g01290"
CDS	join(66055..66654, 66723..67388)	/locus-tag="An18g01290"
		/note="unnamed protein product; Title: strong similarity to hypothetical protein encoded by An13g01340 - Aspergillus niger" /codon-start=1 /protein-id="CAK47203.1" /db-xref="GI:134084170" /translation="MLSLAIQSLLFEADAHAASP ALQRRSSSSASTEGEAVMSPLPSL QTKGLIVISALATVSLICTLSLLTFFTYRFIFWK RHYKRYIGYNQYVVLMFNLILADF IQSLGFIISLRWIQTNSVTASDPACFLQGIWLQI

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                                      GDPMSGLFVLAIAAHTFMHVTLGY
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                                      ESLTRLKRVIFHMALYPVVYICLT
                                      LPLAAGRMASASGHSPSVLYFCFAGSFMTLCGFC
                                      DSLMYTLSRRSVVLEPEARIHGSS
                                      NKYSSRPNKSSVAHHYGNSIDGKGPTNTTIARGR
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                                      /inference="profile:PFAM:PF04299"
                                      /note="unnamed protein product;
                                      Remark: paiB from B. subtilis
                                      seems to be essential. Similarity:
                                      the predicted A. niger protein
                                      shows weak similarity to
                                      transcription regulator 2 of the
                                      pai operon of B. subtilis and
                                      conserved hypothetical proteins
                                      from several procaryotic
                                      organisms. Title: similarity to
                                      transcription regulator paiB
                                      -Bacillus subtilis"
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                                      RIYNPRSEGELGEQASMFLDTQLR
                                      DLTAHCEGEIMGYTTTGTSDTYTHNNPEEKSCPR
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                72467..>73356)
CDS             join(71863..72033,          /locus-tag="An18g01320"
                72097..72406,
                72467..73356)

                                            /EC-number="3.4.23.35"
                                            /inference="profile:PFAM:PF00026"
                                            /note="unnamed protein product;
                                            Function: BAR1 of S. cerevisiae
                                            selectively cleaves the
                                            6-Leu-|-Lys-7 bond in the
                                            pheromone alpha-mating factor.
                                            BAR1 activity is abolished by in
                                            vitro mutation of an aspartic acid
                                            predicted to be in the active
                                            site. Induction: secretion of BAR1
                                            of S. cerevisiae is stimulated to
                                            as much as five times the basal
                                            level by exposure of cells to
                                            alpha-factor. Localization: BAR1
                                            of S. cerevisiae is secreted into
                                            the periplasmic space of MATa
                                            cells. Remark: BAR1 of S.
                                            cerevisiae is already active in
                                            early compartments of the
                                            secretory pathway. Bar1 protease
                                            tolerates large N-terminal
                                            extensions of its substrate and
                                            does not require Golgi-specific
                                            modifications such as outer-chain
                                            glycosylation for activity.
                                            Remark: the protein sequence of
                                            barrier protease BAR1 of S.
                                            cerevisiae is covered by patent
                                            WO9118988-A (AC# AAR20109). the
                                            patented barrier protease is
                                            useful in industrial processes
                                            where leucine-lysine or
                                            leucine-arginine cleavage is
                                            required at low pH or high
                                            temperature. barrier protease may
                                            also be used in the production and
                                            isolation of proteins made by
                                            genetic engineering methods, e. g.
                                            to cleave fusion proteins at
                                            Leu-Arg bonds. Similarity: the
                                            predicted A. niger protein shows
                                            strong similarity to extracellular
                                            protease precursor BAR1 of S.
                                            cerevisiae which belongs to the
                                            subfamily A1 of aspartic-type
                                            peptidases. Title: strong
                                            similarity to extracellular
                                            protease precursor Bar1 -
                                            Saccharomyces cerevisiae
                                            extracellular/secretion proteins"
                                            /citation=[2]
                                            /citation=[3]
                                            /citation=[8]
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                                              GSYNSSASSTYTFVNDEFYIQYVDGSEATGDYVN
                                              DTLKFSNVTLTNFQFAVAYDGDSE
                                              EGVLGIGYASNEASQATVGGGEYTNFPEALVDQG
                                              AINWPAYSLWLDDLDEGKGTILFG
                                              GVNTAKYYGSLQTLPIVSIEDMYVEFAVNLTAVH
                                              LEKNGNSVSVNNSATQFPIPAVLD
                                              SGTALTYIPTSAAASIYEAVGAQYLSEYGYGVIE
                                              CDVKDEDFTFLFDFGSFNMSVDIS
                                              EMILEASSDMTDMNVCTFGLAVIENEALLGDTFL
                                              RSAYVVYDLGNNEISLAKANFNPG
                                              EDHVLEIGTGSDAVPKATGATATGAAATSTASSD
                                              KSDKESSATVPRSQIVSLVAGVLV GVFLVL"
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intron            72407..72466               /locus-tag="An18g01320"
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                                              LNPHPREWAALTKQQENISYISESVDATKCDRLV
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                                              AFQYTLLRFWRSPLHLLFTFVLPL
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                                              VKKTAHTHTELVICVSTIKMTRWLSLMRTIAKVL
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intron	75443..75603	/locus-tag="An18g01330" /number=3
exon	75604..75729	/locus-tag="An18g01330" /number=4
gene	<76028..>77800	/locus-tag="An18g01340"
mRNA	join(<76028..76190, 76240..76393, 76459..>77800)	/locus-tag="An18g01340"
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		/inference="profile:PFAM:PF00328" /note="unnamed protein product; Remark: the patent does not provide further information about the function of the protein, except for a claim of phytase activity. Similarity: the predicted A. niger protein shows strong similarity to protein sequence 11 from patent EP0684313-A/11 and several putative phytases. Title: strong similarity to sequence 11 from patent EP0684313-A - Unclassified organism" /codon-start=1 /protein-id="CAK47207.1" /db-xref="GI:134084174" /translation="MHPTIATLSILAVASLAEAV AIEARSQNATPLTPSPSATTTGID WFQTTPESYQGTTATGVAPFLAETNPAPFGQKTL SPNDPLETSEPIEGAAGRNIFHYM GNLSPYHVPDGFGVDEYPLPKGSNITQMHMIHRH GSRYPSSSEGLASWAQKIINSTAS GNNFTGALSFLNDWDYGLGLEILVPKGRQELYDS GVLNFYNYGHLYNASSPHKLVART TTQDRMLKSAENFLAGFFGLEWTEKANLLPIIEG VGYNNSLIGTYSCTRALEYMAYNA TTPLSTWKNIYLKARTEALRTLTGSYNWTTTDSF NAQDMCAYETISYGYSQFCELFTF EEFENFGYAFDIEFANMVGFACPAGRAQGIAWVE EFLARVEGHLLQTTGTNANMTLDT NPVTFPTDQNLYLDFSHDAGIVAVLTAFGFRQFA ESLPATGPPLYQQFKSSKIVPFAG RTNIEIIKAPNQVAAIRPAGDQSDAYVDGTGETF YVHFLQNQRTLPLHSSFEECEYRD DGWCELSTFMAVQKKGLERSQFEYACFGNWTVTE YGTVTDGVPV"
sig-peptide	76028..76084	/locus-tag="An18g01340" /inference="protein

		motif:SignalP:2.0"
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intron	76394..76458	/locus-tag="An18g01340" /number=2
exon	76459..77800	/locus-tag="An18g01340" /number=3
gene	complement(<77988..>79819)	/locus-tag="An18g01350"
mRNA	complement(join(<77988..78215,78264..78441, 78499..79055, 79113..79172, 79229..79241, 79298..79508, 79560..79700, 79753..>79819))	/locus-tag="An18g01350"
CDS	complement(join(77988..78215,78264..78441, 78499..79055, 79113..79172, 79229..79241, 79298..79508, 79560..79700, 79753..79819))	/locus-tag="An18g01350"
		/inference="profile:COGS:COG2141" /note="unnamed protein product; Remark: HA protein regulates homeostasis and adaptation. the C. glutamicum HA genes (I) can be used in vectors for expression in host cells and production of fine chemicals, such as, an organic acid, proteinogenic or nonproteinogenic amino acid (preferred), purine or pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor, polyketide or enzyme. the amino acids produced can be lysine, glutamine, glutamate,alanine, aspartate, glycine, serine, threonine, methionine,cysteine, valine, leucine, isoleucine, arginine, proline,histidine, tyrosine, phenylalanine, or tryptophan. the fine chemical production can be modulated. the presence of (I) or HA proteins encoded by then are used for diagnosing the presence or activity of Corynebacterium

diphtheriae. (I) can be used to map the C. glutamicum genome or can be used as markers for genetically engineered Corynebacterium or Brevibacterium. the HA proteins encoded by the (I) are used to maintain homeostasis in C. glutamicum or help the microorganism to adapt to different environmental conditions. Similarity: the predicted A. niger protein shows strong similarity to HA protein sequence SEQ ID NO:420 from patent WO200100842-A2 (AC# AAB79232), which is a monooxygenase by similarity. Title: strong similarity to HA protein sequence SEQ ID NO:420 from patent WO200100842-A2 - Corynebacterium glutamicum"
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                81343..81426,
                81473..81659,
                81704..81754,
                81802..81972,
                82019..82337,
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                                               sequence:UniProtKB:SCDURIII.1"
                                               /note="unnamed protein product;
                                               Function: S. cerevisiae DUR3 is a
                                               urea symporter mediating urea
                                               import. Induction: high-level
                                               expression of S. cerevisiae DUR3
                                               is inducer dependent, requiring
                                               functional DAL81 and DAL82 genes.
                                               Regulation: expression of S.
                                               cerevisiae DUR3 is regulated in a
```

manner similar to that of other
genes in the allantoin pathway.
Repression: DUR3 expression is
highly sensitive to nitrogen
catabolite repression and also has
a partial requirement for the GLN3
product. Repression: maintenance
of S. cerevisiae DUR3 mRNA at
uninduced, nonrepressed basal
levels requires the negatively
acting DAL80 gene product.
Similarity: S. cerevisiae DUR3
belongs to the major facilitator
family. Title: strong similarity
to urea transport protein Dur3 -
Saccharomyces cerevisiae plasma
membrane"
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PFWFAAGCSPMIVFFALIGISYKRKIPDAHTSLE
VVRIRYGRIAHAVFMTLCLINNIF
ACANMLLGAAAVISAITGMHIIAATFLLPVGVTV
YTFVGGIKATFLTDYFHTAIILII
ACYLSVKAFTFEEVGSIGKLYELVQAAAQRHPVS
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SNFGLVIMDTSYFIKAFSAAPSSVVPGYTIGGIA
YFAIPWALGTIMSSLALGLENTAS
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SFDVYREYINRAASDRDIIRASHFGVIFFAAFSA
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VWLGTAQHFYGAVSVSSTGQILPC
VYGTVASAFSPIVYSVLITLVKPQRYDWAEFRKE
KLGLERLDSDSDITVNGQGSEEQQ
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Remark: mutagenesis experiments demonstrate that conserved amino acid residues, functionally critical in the human cystic fibrosis transmembrane conductance regulator (hCFTR), play a vital role in YCF1-mediated cadmium resistance. Remark: substitution of a serine to alanine residue in a potential protein kinase A phosphorylation site in a central region of YCF1, which displays sequence similarity to the central regulatory domain of hCFTR, also rendered YCF1 nonfunctional. Remark: the YCF1 gene of S. cerevisiae is an MgATP-energized, uncoupler-insensitive vacuolar membrane glutathione S-conjugate transporter. Similarity: the predicted A. niger protein shows strong similarity to cadmium factor (YCF1) from S. cerevisiae, which belongs to the ATP binding cassette (ABC) protein superfamily of membrane transporters. Title: strong similarity to cadmium resistance protein Ycf1 – Saccharomyces cerevisiae [putative sequencing error] putative sequencing error"
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                                        activator ACE1 play a key role in
                                        mediating copper resistance in S.
                                        cerevisiae. Similarity: the
                                        predicted A. niger protein shows
                                        similarity to the copper
                                        homeostasis protein CUP9 from S.
                                        cerevisiae. the predicted A. niger
                                        protein shows strong similarity to
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Function: the MCT3 transporter
from Rattus norvegicus is a
proton-linked monocarboxylate
transporter. it catalyzes the
rapid transport across the plasma
membrane of many monocarboxylates
such as lactate,
pyruvate,branched-chain oxo acids
derived from leucine, valine and
isoleucine, and the ketone bodies
acetoacetate,beta-hydroxybutyrate
and acetate. Similarity: the
predicted A. niger protein shows
strong similarity to the
monocarboxylate transporter 3
(MCT3) of R. norvegicus, which
belongs to the major facilitator
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transporter 3 MCT3 - Rattus
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                                    Catalytic activity: alcohol + NAD+
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                                    Pathway: alcohol dehydrogenase
                                    ADH-T from B. stearothermophilus
                                    is involved in glycolysis /
                                    gluconeogenesis; fatty acid
                                    metabolism; bile acid
                                    biosynthesis; tyrosine metabolism;
                                    glycerolipid metabolism. Remark:
                                    the protein sequence of alcohol
                                    dehydrogenase ADH-T from B.
                                    stearothermophilus NCA1503 is
                                    covered by patent JP04218378-A
                                    (AC# AAR26874). Similarity: the
                                    predicted A. niger protein shows
                                    strong similarity to thermostable
                                    alcohol dehydrogenase ADH-T from
                                    B. stearothermophilus NCA1503,
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                                           KKFLLRQWIPAQGGREQQPESLILSPVRKNLPSI
                                           SVDGILLHAALLTVNLILKLGGWP
                                           GLLKFMLRTFAISSVLAPIGLIGFLFLVSFTPRN
                                           IKSLSKDKSVIGKPLLFPITLDHT
                                           RLSPIKNNFTFNVLFVGIPVGISCRFGRLLSIDA
                                           KHTDEEECTERSSLLRLLQTYFSS
                                           WFSFDSARYLHRGDDTLSLENKLNKFLREQNENP
                                           AKWPYAYMLSVPRFLWWERSVVTW
                                           WYLYSESKELDAVIMEINNSFDEKRNVLFKVRRT
                                           RIYTESPEKGFEQLLDCKEEHLDE
                                           DKRVFSLIPQHGKYAYKATWKKEIFSSPFEKVGE
                                           TVSSTFLDPVVPSSWSGNRSLSNT
                                           TTFDPSGAPRMIARLWCKVPPIDPGKASSFQIFS
                                           ILLIWTVNVTLATPRILFQAIRLH
                                           VMNLMRMMEHPDVRPGSEPRRPSKGERKDAPLKM
                                           LHSLFDLHANLQSRMLERFFREYL
```

```
                                      KHIVASYPGDLEVTYIPCKSVFKTTICLRSTQYS
                                      AEGQDPRRLRLEVMDPAFYSRIVN
                                      SPNAGTAMAKETKPGRSPADALSSPVIASDITQS
                                      LQLLDVTVSENRTYDKACSRISSW
                                      VLCLRRWLTSSFMDSFVCKALPPRTQEEYVSCLI
                                      QLWLEKLTWDFLSPHQIYRVIRAA
                                      MLQWAICWILF"
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exon	101875..101958	/locus-tag="An18g01440" /number=1
intron	101959..102202	/locus-tag="An18g01440" /number=1
exon	102203..102219	/locus-tag="An18g01440" /number=2
intron	102220..102258	/locus-tag="An18g01440" /number=2
exon	102259..102360	/locus-tag="An18g01440" /number=3
intron	102361..102391	/locus-tag="An18g01440" /number=3
exon	102392..102399	/locus-tag="An18g01440" /number=4
intron	102400..102620	/locus-tag="An18g01440" /number=4
exon	102621..103153	/locus-tag="An18g01440" /number=5
intron	103154..103204	/locus-tag="An18g01440" /number=5
exon	103205..104542	/locus-tag="An18g01440" /number=6
gene	<106231..>106803	/locus-tag="An18g01450"
mRNA	join(<106231..106565, 106647..>106803)	/locus-tag="An18g01450"
CDS	join(106231..106565, 106647..106803)	/locus-tag="An18g01450"

```
                                      /EC-number="1.14.-.-"
                                      /note="unnamed protein product;
                                      Function: ordA of A. parasiticus
                                      is involved in the aflatoxin
                                      biosynthesis and converts
                                      O-methylsterigmatocystin (OMST) to
                                      aflatoxins B1 or G1 and converts
                                      dihydro-O-methylsterigmatocystin
                                      (DHOMST) to aflatoxins B2 or G2.
                                      Remark: aflatoxins comprise a
                                      group of polyketide-derived
                                      carcinogenic mycotoxins. Remark:
                                      it is assumed that the ORF is
                                      N-terminally shorter and has
                                      another start codon 5' to the
                                      predicted one ; the ORF is around
                                      400 amino acids shorter than most
                                      of the homologues cytochrome p450
                                      proteins. Remark: ordA of A.
                                      parasiticus is also called
                                      cytochrome p450 64, cyp64 or omst
                                      oxidoreductase. Similarity: the
                                      ORF shows similarity to several
                                      cytochrome P450 related proteins
                                      from different species. Title:
                                      strong similarity to
                                      O-methylsterigmatocystin
                                      oxidoreductase ordA - Aspergillus
```

exon	106231..106565	/locus-tag="An18g01450" /number=1
intron	106566..106646	/locus-tag="An18g01450" /number=1
exon	106647..106803	/locus-tag="An18g01450" /number=2
gene	<107279..>108340	/locus-tag="An18g01460"
mRNA	join(<107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..>108340)	/locus-tag="An18g01460"
CDS	join(107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..108340)	/locus-tag="An18g01460"

/EC-number="1.-.-.-"
/inference="profile:COGS:COG1028"
/inference="profile:PFAM:PF00106"
/note="unnamed protein product;
Catalytic activity: cyclohexanol
dehydrogenases convert
cyclohexanol + NAD(+) <=>
cyclohexanone + NADH. Function:
chnA of A. sp. is an alcohol
dehydrogenases proposed to
catalyze the conversion of
cyclohexanol to cyclohexanone (EC
1. 1. 1. 245). Phenotype:
cyclohexanol was detected as the
major intermediate accumulated in
the chnA mutant of A. sp. Remark:
chnA of A. sp. is encoded in the
gene cluster for cyclohexanol
oxidation. Similarity: the ORF
shows similarity to several
dehydrogenases from different
species and with various
specificities. Title: strong
similarity to cyclohexanol
dehydrogenase chnA - Acinetobacter
sp"
/citation=[57]
/codon-start=1
/protein-id="CAK47219.1"
/db-xref="GI:134084186"
/translation="MAHLLQGTAFITGAGSGIGA
GVARTFIQNGISKLALVDINLSIL

```
                                          QKVSESLKQTFPNVELLTSAVDVTNEVHVDNAVQ
                                          KAATTFGRVDIGVNSAGVGDPGEP
                                          TDRLSLKDWQRTVHINQTGVWLSQRALIQQMLTQ
                                          KSRGTRHGRGVIVNVCSSLGITAS
                                          ATGIPFPAYTSSKHGVMGLTKMDAKYYAPSGIRI
                                          NAVCPGFVDTPMVSKAVDSGVFKK
                                          EVESAPVGRIGDVEEITDSILFLASPMSSFIYGA
                                          GLVVDGGYGL"
sig-peptide      join(107279..107327,     /locus-tag="An18g01460"
                 107380..107387)
                                          /inference="protein
                                          motif:SignalP:2.0"
mat-peptide      join(107388..107740,     /locus-tag="An18g01460"
                 107795..107907,
                 107966..107988,
                 108045..108097,
                 108151..108337)
                                          /product="unnamed"
exon             107279..107327           /locus-tag="An18g01460"
                                          /number=1
intron           107328..107379           /locus-tag="An18g01460"
                                          /number=1
exon             107380..107740           /locus-tag="An18g01460"
                                          /number=2
intron           107741..107794           /locus-tag="An18g01460"
                                          /number=2
exon             107795..107907           /locus-tag="An18g01460"
                                          /number=3
intron           107908..107965           /locus-tag="An18g01460"
                                          /number=3
exon             107966..107988           /locus-tag="An18g01460"
                                          /number=4
intron           107989..108044           /locus-tag="An18g01460"
                                          /number=4
exon             108045..108097           /locus-tag="An18g01460"
                                          /number=5
intron           108098..108150           /locus-tag="An18g01460"
                                          /number=5
exon             108151..108340           /locus-tag="An18g01460"
                                          /number=6
gene             <108826..>111209         /locus-tag="An18g01470"
mRNA             join(<108826..108944,    /locus-tag="An18g01470"
                 109020..109023,
                 109089..109305,
                 109377..109778,
                 109841..109905,
                 110160..110181,
                 110244..110293,
                 110355..110492,
                 110524..110752,
                 110866..110960,
                 111135..>111209)
CDS              join(108826..108944,     /locus-tag="An18g01470"
                 109020..109023,
                 109089..109305,
                 109377..109778,
                 109841..109905,
                 110160..110181,
                 110244..110293,
                 110355..110492,
                 110524..110752,
                 110866..110960,
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```
                   111135..111209)
                                          /EC-number="1.14.-.-"
                                          /inference="profile:COGS:COG0493"
                                          /note="unnamed protein product;
                                          Remark: aflatoxins are
                                          polyketide-derived secondary
                                          metabolites. Remark: moxY of A.
                                          parasiticus is expressed
                                          concurrently with genes involved
                                          in aflatoxin biosynthesis and it
                                          lies on one end of the cluster of
                                          this genes. Therefore moxY of A.
                                          parasiticus is presumably also
                                          involved in aflatoxin
                                          biosynthesis. Similarity: the ORF
                                          shows similarity to monooxigenases
                                          from several species and with
                                          different functions. Title: strong
                                          similarity to monooxygenase moxY
                                          -Aspergillus parasiticus"
                                          /citation=[55]
                                          /codon-start=1
                                          /protein-id="CAK47220.1"
                                          /db-xref="GI:134084187"
                                          /translation="MANEQTCSPSINLNTHENMC
                                          KGRIQQRRYPATCNMLKKPRCVPH
                                          TQIELCTVLFAFSNMISASTTDTFTQVIIIGAGM
                                          SGLAMACQLKKQLCCEDFVIYDRA
                                          PSFGGTWYFNKCCGVDIPAAFYSFSFALYPQFTC
                                          FFPKQEEILQYIHGVADEFSVALK
                                          LVGHTEWEGADWQDSEQCWEVRLREIPSGRKFTR
                                          RCRILISAVGGLTNPKHVMLQGIE
                                          RFQGNIVHTALWDQETAVAGKNVIVIGNGASATQ
                                          FIPAIADDAASINQFIRHVRKCAP
                                          EEQYWSLLTPEYSIGCKRRVFDNDGYLKCLHRPN
                                          VDITNDPVVAVEEQSITTQSGKRF
                                          PADLIADVDLDYGRCLRLGSLSRSTMSTGEVVMG
                                          VRDKNIGTVSAAYKHLRRWPWRNF
                                          LTFSTFSDPTLAGAIHQLSIQLKVSVVIKQASEE
                                          RFNTKLKSALRKTVFTNMCRSLPA
                                          STISLVRVLTVVEEKPSLSLL"
exon           108826..108944             /locus-tag="An18g01470"
                                          /number=1
intron         108945..109019             /locus-tag="An18g01470"
                                          /number=1
exon           109020..109023             /locus-tag="An18g01470"
                                          /number=2
intron         109024..109088             /locus-tag="An18g01470"
                                          /number=2
exon           109089..109305             /locus-tag="An18g01470"
                                          /number=3
intron         109306..109376             /locus-tag="An18g01470"
                                          /number=3
exon           109377..109778             /locus-tag="An18g01470"
                                          /number=4
intron         109779..109840             /locus-tag="An18g01470"
                                          /number=4
exon           109841..109905             /locus-tag="An18g01470"
                                          /number=5
intron         109906..110159             /locus-tag="An18g01470"
                                          /number=5
exon           110160..110181             /locus-tag="An18g01470"
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                                                /number=6
intron          110182..110243                 /locus-tag="An18g01470"
                                                /number=6
exon            110244..110293                 /locus-tag="An18g01470"
                                                /number=7
intron          110294..110354                 /locus-tag="An18g01470"
                                                /number=7
exon            110355..110492                 /locus-tag="An18g01470"
                                                /number=8
intron          110493..110523                 /locus-tag="An18g01470"
                                                /number=8
exon            110524..110752                 /locus-tag="An18g01470"
                                                /number=9
intron          110753..110865                 /locus-tag="An18g01470"
                                                /number=9
exon            110866..110960                 /locus-tag="An18g01470"
                                                /number=10
intron          110961..111134                 /locus-tag="An18g01470"
                                                /number=10
exon            111135..111209                 /locus-tag="An18g01470"
                                                /number=11
gene            <111907..>113460               /locus-tag="An18g01480"
mRNA            <111907..>113460               /locus-tag="An18g01480"
CDS             111907..113460                 /locus-tag="An18g01480"
                                                /inference="profile:COGS:COG2124"
                                                /inference="profile:PFAM:PF00067"
                                                /inference="similar to AA
                                                sequence:UniProtKB:AB013443.1"
                                                /note="unnamed protein product;
                                                Function: eln2 of C. cinereus
                                                encodes a novel type of microsomal
                                                cytochrome P450 enzyme, with is
                                                involved in mushroom
                                                morphogenesis. Phenotype: a
                                                dominant mutation of the
                                                elongationless2 (eln2) gene of the
                                                mushroom C. cinereus affects
                                                pattern formation in the
                                                development of fruit body
                                                primordia, causing dumpy primordia
                                                which culminate in mature fruit
                                                bodies with short stipes.
                                                Similarity: the ORF shows
                                                similarity to several cytochrome
                                                p450 related proteins from
                                                different species,which have
                                                different cellular functions.
                                                Title: strong similarity to
                                                cytochrome p450 related protein
                                                eln2 - Coprinus cinereus"
                                                /citation=[54]
                                                /codon-start=1
                                                /protein-id="CAK47221.1"
                                                /db-xref="GI:134084188"
                                                /translation="MPTILLTLLALLTLRLLYEY
                                                KRDRNLPPGPRRLPLIGNLHQAPQ
                                                TLPWRVFDQWSKTYGPIMSAQFGRQTLILITSPT
                                                IARDLLDKRGSIYADRPDLVMANN
                                                ITKGLHMLIRQYDDWLRLHQRLDAPLLSPRASNT
                                                YHPIQDLESKQLMFDLLRSNDFDA
                                                HFERYSGSLMFALAYGFRLLSPKGQELRDMRTIQ
                                                GNFTYAARVGTWIVDAIPVLNYLP
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                                        AVVAPWKRLAEKLFKLEASVHTRHLEKGLNSEPW
                                        NWSKEFAASKHAEGMPRLDLAYNL
                                        GILVDAGFETTWTVMKIFVLAMRSDPRFVAVARK
                                        ELDEVVGEDRMPTFEDQEKLVYIQ
                                        AVVDETLRWRSMAPGGIPHAARKEDTYMGYRIPK
                                        GATVIPLFWSMCLTDEPWDDPLEF
                                        RPERWFEATEKEEGRFRNFFGYGRRICTGRHIAR
                                        NSLFLLMARILWAFDIQAPLGDDG
                                        KPVPVDDMAFDSAFVSTPEPFEALFVPRSEKTKE
                                        IVEREWNEMEKDMAVLMGQVRDSQ
                                        RALGLDVRA"
sig-peptide     111907..111957         /locus-tag="An18g01480"
                                        /inference="protein
                                        motif:SignalP:2.0"
mat-peptide     111958..113457         /locus-tag="An18g01480"
                                        /product="unnamed"
exon            111907..113460         /locus-tag="An18g01480"
                                        /number=1
gene            complement(<113565..>11 /locus-tag="An18g01490"
                4733)
mRNA            complement(join(<113565 /locus-tag="An18g01490"
                ..114153,
                114210..>114733))
CDS             complement(join(113565. /locus-tag="An18g01490"
                .114153,
                114210..114733))
                                        /inference="profile:COGS:COG0598"
                                        /inference="profile:PFAM:PF01544"
                                        /inference="similar to AA
                                        sequence:UniProtKB:SC41293.1"
                                        /note="unnamed protein product;
                                        Function: alr2 of S. cerevisiae is
                                        an uptake transporter for
                                        inorganic cations, e. g.
                                        magnesium, which presence seems to
                                        be important for resistance to the
                                        toxic effect of aluminum. Remark:
                                        alr2 of S. cerevisiae is also
                                        called YFL050C. Similarity: the
                                        predicted ORF is 395 amino acids
                                        shorter at the N-terminus and 57
                                        amino acids shorter at its
                                        C-terminal end than alr2 of S.
                                        cerevisiae (nearly the same is
                                        true for alr1 of S. cerevisiae).
                                        Title: strong similarity to ion
                                        transporter Alr2 -Saccharomyces
                                        cerevisiae plasma membrane"
                                        /citation=[40]
                                        /codon-start=1
                                        /protein-id="CAK47222.1"
                                        /db-xref="GI:134084189"
                                        /translation="MSSDSTPDPRLEKPRVAVAS
                                        RLNFFTSQLNTSIEASSIEDLCSV
                                        YRPFELLLETGAHSGLWWLDITAPSEEDIEALAR
                                        FFNLHPLTTEDIKTRETREKIELF
                                        GQYYFLSLRPPRRLETDTGVRIVSHNLYAVVFRG
                                        GVLSFSFDPSLHTSHVRQRIKEHS
                                        SHLLLTSDWICYALIDDIVDGFAPFISRVENGVV
                                        TVEDSVSITRPDDMGLALQRIFKL
                                        RKEVMNIRQPLHDKIDVIRSFARHCDISDTSSSQ
                                        VALYLSDICDHVVTMIANLEQAEQ
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                                   MLSRLQSKYLTQVHFDSGRMRNGIASALSKLTVL
                                   ASILVPMQFITGLFGMNVRVPGKT
                                   HDGDNSLTWWFSILGFILGLTVIFAWVAKRIGLL
                                   DR"
exon          complement(113565..1141   /locus-tag="An18g01490"
              53)
                                   /number=1
intron        complement(114154..1142   /locus-tag="An18g01490"
              09)
                                   /number=1
exon          complement(114210..1147   /locus-tag="An18g01490"
              33)
                                   /number=2
gene          complement(<115549..>11   /locus-tag="An18g01500"
              6444)
mRNA          complement(join(<115549   /locus-tag="An18g01500"
              ..115734,
              115791..116016,
              116080..>116444))
CDS           complement(join(115549.   /locus-tag="An18g01500"
              .115734,115791..116016,
              116080..116444))
                                   /note="unnamed protein product;
                                   Title: strong similarity to
                                   hypothetical protein encoded by
                                   An15g02540 - Aspergillus niger"
                                   /codon-start=1
                                   /protein-id="CAK47223.1"
                                   /db-xref="GI:134084190"
                                   /translation="MSDQQLLLERQARRHALAKV
                                   EEHIKQTPNMHVEPSDLKAASIRH
                                   FPLSLEGTKDQPWFFRPYEEELPLPVEEAEFLQI
                                   ELTPDNIMWDTRALELFLFDHFHD
                                   CRGFAKCEYPQNPPYGVYREIGDVKFGQLLECGK
                                   FNWYAVSVTDYPGENLPHIKAIVE
                                   NDAIGDDKLLRGEIMTITDIMKARLRSNTLRPHI
                                   VAPMLVLSLMGPRHARVLEADFDG
                                   VMLNIRASGLYDFTRKNTDAVQLLTRYWLGGACG
                                   QTTKKS"
exon          complement(115549..1157   /locus-tag="An18g01500"
              34)
                                   /number=1
intron        complement(115735..1157   /locus-tag="An18g01500"
              90)
                                   /number=1
exon          complement(115791..1160   /locus-tag="An18g01500"
              16)
                                   /number=2
intron        complement(116017..1160   /locus-tag="An18g01500"
              79)
                                   /number=2
exon          complement(116080..1164   /locus-tag="An18g01500"
              44)
                                   /number=3
gene          complement(<117672..>11   /locus-tag="An18g01510"
              8234)
mRNA          complement(join(<117672   /locus-tag="An18g01510"
              ..117782,
              117885..118021,
              118123..>118234))
CDS           complement(join(117672.   /locus-tag="An18g01510"
              .117782,117885..118021,
```

```
                    118123..118234))
                                              /note="unnamed protein product;
                                              Remark: the ORF is questionable
                                              due to its suboptimal intron-exon
                                              structure and short lenght Title:
                                              questionable ORF"
                                              /codon-start=1
                                              /protein-id="CAK47224.1"
                                              /db-xref="GI:134084191"
                                              /translation="MREQDNDRFMLPITLPNHCH
                                              SGSDVGLPPFACQSLGWQTNAVLG
                                              PVYGKFAESIAIILLCIFGQWDEDLVTRGNIIIS
                                              GVDGETLTKVLLPVLTMKRTWLKG
                                              YHLLIGGVAVCLCVCFV"
     exon               complement(117672..1177  /locus-tag="An18g01510"
                        82)
                                              /number=1
     intron             complement(117783..1178  /locus-tag="An18g01510"
                        84)
                                              /number=1
     exon               complement(117885..1180  /locus-tag="An18g01510"
                        21)
                                              /number=2
     intron             complement(118022..1181  /locus-tag="An18g01510"
                        22)
                                              /number=2
     exon               complement(118123..1182  /locus-tag="An18g01510"
                        34)
                                              /number=3
     gene               <119176..>120297         /locus-tag="An18g01520"
     mRNA               <119176..>120297         /locus-tag="An18g01520"
     CDS                119176..120297           /locus-tag="An18g01520"
                                              /EC-number="1.-.-.-"
                                              /inference="profile:COGS:COG0673"
                                              /inference="profile:PFAM:PF01408"
                                              /inference="similar to AA
                                              sequence:UniProtKB:ENQUTCH.2"
                                              /note="unnamed protein product;
                                              Function: due to the presence of a
                                              putative 'zinc cluster' motif and
                                              its low (16%) but significant
                                              similarity with the DNA-directed
                                              DNA polymerase of hepatitis B
                                              virus,it was assumed that qutH of
                                              A. nidulans is a DNA-binding
                                              protein, which is possibly
                                              involved in the regulation of
                                              genes essential for the
                                              utilisation of protocatechuic
                                              acid. Function: due to the
                                              similarity of the ORF to
                                              oxidoreductases, it is here
                                              assumed that the ORF is encoding a
                                              protein with oxidoreductase
                                              activity. Similarity: the ORF
                                              shows similarity to several
                                              oxidoreductases from different
                                              species. Title: strong similarity
                                              to quinic-acid utilisation gene
                                              qutH - Aspergillus nidulans"
                                              /citation=[10]
                                              /codon-start=1
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                                            /protein-id="CAK47225.1"
                                            /db-xref="GI:134084192"
                                            /translation="MLNVIIVGAGLIGPRHAQSV
                                            ITNPSTNLLALVDPSPSASSVAKT
                                            LNTLYFPSLSALLSSVPNIPHPDAAIICTPNHTH
                                            VPVALELISHNIHILLEKPISDTI
                                            TTALPLLQAQQKYPDVKILIGHHRRFNPYITKTK
                                            EILESGSLGPIIALSGLWTLYKPA
                                            SYFTGATEWRRDKAKGGVLSINLIHDVDLLHYLF
                                            GPITRVYAEKTLPQRGGPDGNENH
                                            TAEEGAAITFRFASGVVGTFVVSDCAPSPWNFEA
                                            GTGENPIIPKVGGVGGGLYRVLGS
                                            RGSLSVPDLKRWSYDGVEGEKGWNQRLQVEEFEV
                                            DEGVPFDLQLEHFVRVLERGETPR
                                            CDAVEGLRALVVVDAVKRAMETEEVVKVESVEEI
                                            LARNE"
sig-peptide      119176..119226             /locus-tag="An18g01520"
                                            /inference="protein
                                            motif:SignalP:2.0"
mat-peptide      119227..120294             /locus-tag="An18g01520"
                                            /product="unnamed"
exon             119176..120297             /locus-tag="An18g01520"
                                            /number=1
gene             complement(<120373..>12    /locus-tag="An18g01530"
                 1787)
mRNA             complement(join(<120373    /locus-tag="An18g01530"
                 ..120856,
                 120912..121419,
                 121479..121515,
                 121584..>121787))
CDS              complement(join(120373.    /locus-tag="An18g01530"
                 .120856,120912..121419,
                 121479..121515,
                 121584..121787))
                                            /note="unnamed protein product;
                                            Function: pth11 of M. grisea is
                                            involved in host surface
                                            recognition for the initiation of
                                            appressorium formation, which is
                                            important in plant infection.
                                            Phenotype: M. grisea pth11 mutants
                                            are nonpathogenic due to a defect
                                            in appressorium differentiation.
                                            Remark: on the same contig another
                                            ORF shows similarity to pth11 of
                                            M. grisea, see 130cg. Similarity:
                                            the ORF is 85 amino acids shorter
                                            at its N-terminus and 155 amino
                                            acids shorter at the C-terminal
                                            end than pth11 of M. grisea.
                                            Title: strong similarity to
                                            integral membrane protein PTH11 -
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```

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                                       VASIVRIYSVDQFTKRTDVTWTLG
                                       PVFIWSTIEPGLSLVCACLPHLAPLVRLAHIKLS
                                       SSQDSKRSRPTNPSTPWRSRSGNA
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mRNA            <122486..>123895           /locus-tag="An18g01540"
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                                           /inference="similar to AA
                                           sequence:UniProtKB:AB014491.1"
                                           /note="unnamed protein product;
                                           Function: TRI101 of F.
                                           sporotrichioides conferred
                                           significant increased tolerance to
                                           the mycotoxin DAS (trichothecene
                                           4,15-diacetoxyscirpenol), which is
                                           harmful for vertebrates. Function:
                                           TRI101 of F. sporotrichioides
                                           converts isotrichodermol to
                                           isotrichodermin and is required
                                           for the modification of T-2 toxin,
                                           which inhibits protein synthesis
                                           in eukaryotes. Phenotype: TRI101
                                           mutants of F. sporotrichioides
                                           were altered in their abilities to
                                           synthesize T-2 toxin and
                                           accumulated isotrichodermol and
                                           small amounts of
                                           3,15-didecalonectrin and
                                           3-decalonectrin, trichothecenes.
                                           Title: strong similarity to
                                           trichothecene
                                           3-O-acetyltransferase TRI101 -
                                           Fusarium sporotrichioides"
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                                        ELKTQHFPVAAFNADTLCRRDIWPTDLGEHLPIS
                                        LVQANFIRGGLILTWCILHMAGDG
                                        NSFQTWMRVWAEECRRAQGVKITDPVVLPPAIFA
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                                        LPFKPPEGLPPKMLAKNHRAQVFYFSPEALAALK
                                        KEASPKNASEPRDVPWISTNDALS
                                        ALLWRTVMAVQWPLETLESVNQDQESFFNIALNG
                                        RLRTDPPVHPNTLGCFLEYIGVSM
                                        PVHKMLTSAQLANLAVLIRQALHQVSNQHTDDVI
                                        SLIEQLDDIRKIFPASLVDLPGFN
                                        CILTSWVDFALYNLDWGTLLGGHIESVRAPHVGV
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mRNA              complement(join(<123984 /locus-tag="An18g01550"
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                  125913..>127145))
CDS               complement(join(123984. /locus-tag="An18g01550"
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                  125485..125732,
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                                        protein AAM43672.1 - Dictyostelium
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                                        QNPLWQQQMDDVVDDAVTGLGLTAQSDEVQAELY
                                        KLLIYEEGAFFLPHQDTEKADGMF
                                        ATLVVCLPSKHEGGTLVASHRGWKIAWSTASSSE
                                        FSFSWAAWYADVIHEVRPVTSGYR
                                        VALVYNLIHRPLVGLGISGVQTDKLTHLLESWVS
                                        DCSGNGQSDHSAWDHHINGDCPPA
                                        LVYVLEHQYTVVELSFDRLKGVDQVRFGELQKAC
                                        QGLDFDLYLANIEKTRMGGVDGRY
                                        GNSYWKAHNALEDVLGGNQKFLSVVDASGSEVGK
                                        RLPFHGKLLIQEDFFSNRLPDDEK
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                                          FFRGFRVQYKHTSNSGLEFAANCRPTKHTTSIRI
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                                          YVLPAPLVPPDWKGRSCILCRCYTCASLDTFIED
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                                          FFFTKTVVGPVGMQMLRIWKTDAMMLVSQLHAWN
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exon              complement(125485..1257    /locus-tag="An18g01550"
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exon              complement(125913..1271    /locus-tag="An18g01550"
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mRNA              join(<127862..127973,      /locus-tag="An18g01560"
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                  128777..128854,
                  128935..129026,
                  129125..129230)
                                             /note="unnamed protein product;
                                             Remark: the ORF is questionable
                                             due to its suboptimal intron-exon
                                             structure. Title: questionable
                                             ORF"
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                                           DWRSVASSGDEGKSEFPDGVWTGQ
                                           ALESIANMQLRGLPLRVPGDFRQFHPPLLFSLAK
                                           DFFIPVDVANSITAKPPETIPGQS
                                           LSAISPFLSCGQMRGTNAVGSPDPLSGKSCASHQ
                                           RVSASTLAFRTGGSRIPGYRTEEQ
                                           MATPCHEPWLSRRARRIPNVY"
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exon            128310..128432             /locus-tag="An18g01560"
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intron          128433..128565             /locus-tag="An18g01560"
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exon            128566..128684             /locus-tag="An18g01560"
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exon            129125..129230             /locus-tag="An18g01560"
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mRNA            join(<129407..129556,      /locus-tag="An18g01570"
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                130176..130256,
                130321..130729,
                130866..>130916)
CDS             join(129407..129556,       /locus-tag="An18g01570"
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                130008..130130,
                130176..130256,
                130321..130729,
                130866..130916)
                                           /note="unnamed protein product;
                                           Function: pth11 of M. grisea pth11
                                           is involved in host surface
                                           recognition for the initiation of
                                           appressorium formation, which is
                                           important in plant infection.
                                           Phenotype: M. grisea pth11 mutants
                                           are nonpathogenic due to a defect
                                           in appressorium differentiation.
```

Remark: on the same contig another
ORF shows strong similarity to
pth11 of M. grisea, see 160wg.
Similarity: the ORF is 92 amino
acids shorter at the N-terminal
end and 165 amino acid its
C-terminus than pth11 of M.
grisea. Title: similarity to
integral membrane protein PTH11 -
Magnaporthe grisea"
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IPIKLSISWMLIRVAEGRKAYLYAQYVVIVVFVL
MNIIALIFILINCIPVDAAWNTEL
LKQGGHCQPSYVLADVYYACTAVNILTDWVTALM
PVPLLWNVQLNRNTKISIVGLMGL
GIFASMSACVRLKYTVALTSQSNYLYSVTNVVIW
GFTENALGMIVGNVATLRPLFRIL
RDRKTSSNNKYNSRGYYSSQRTGPANMYSRNYEL
AEQGKHTNQITTTSMADHTRRPSQ
MSDGDSQKQILAGGTPPGDTDILKKELNDSLQLQ
FSKQA"

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exon	130008..130130	/locus-tag="An18g01570" /number=4
intron	130131..130175	/locus-tag="An18g01570" /number=4
exon	130176..130256	/locus-tag="An18g01570" /number=5
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exon	130321..130729	/locus-tag="An18g01570" /number=6

intron	130730..130865	/locus-tag="An18g01570"
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exon	130866..130916	/locus-tag="An18g01570"
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mRNA	complement(join(<131646	/locus-tag="An18g01580"
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	132363..>132375))	
CDS	complement(join(131646.	/locus-tag="An18g01580"
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	132363..132375))	
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		/inference="profile:PFAM:PF00484"
		/inference="similar to AA
		sequence:UniProtKB:AB040135.1"
		/note="unnamed protein product;
		Catalytic activity: pca1 of P.
		purpureum converts H(2)CO(3) <=>
		CO(2) + H(2)O with the usage of
		zinc as cofactor. Function:
		carbonic anhydrases catalyze the
		reversible hydration of carbon
		dioxide. Remark: an alternate name
		for pca1 of P. purpureum is
		gtpca1. Similarity: the ORF shows
		similarity to several carbonic
		anhydrases from different species
		and with various cellular
		functions. Title: strong
		similarity to carbonic anhydrase
		pca1 – Porphyridium purpureum"
		/citation=[32]
		/citation=[62]
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		/db-xref="GI:134084198"
		/translation="MAVTDLHSQQPEKPQDPYTK
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		RAQHPQILWIGCSDSRCPETTLLDLKPGDVFVHR
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		KVKHVVVCGHTCCGGVGAVLAAPKGERDGEDGEK
		SVLDAWLSSLKRVRDRYASELEGI
		HGEYERGVRLVELNVLEGVRVLMAMGVVREAVEK
		GEVEVHGAVYNVGCGVVRELELEV KL"
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intron	complement(132296..1323	/locus-tag="An18g01580"
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mRNA	complement(join(<133082	/locus-tag="An18g01590"
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	135000..135045,	
	135113..>135202))	

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                                           /note="unnamed protein product;
                                           Catalytic activity: cat2 of C.
                                           tropicalis catalyses acetyl-CoA +
                                           carnitine <=> CoA +
                                           O-acetylcarnitine. Function: cat2
                                           of C. tropicalis is specific for
                                           the acetylation of short chain
                                           fatty acids and may also be
                                           involved in the transport of
                                           acety-CoA into mitochondria.
                                           Similarity: the ORF overlaps with
                                           A. niger EST EMBLEST:BE760390.
                                           Title: strong similarity to
                                           carnitine O-acetyltransferase cat2
                                           - Candida tropicalis inner
                                           membrane"
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                                           RDPAKRAASVATAALEFKRQVDDGSLEPEYMRGQ
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                                           RWFDKPLQFIINDNGTAGFMGEHSMMDGSPTHRM
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                                           IRTVSDESVAFCKAISDPAVPREE
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                                           LLREGEKLPALYEDPAFAYSSSWY
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                                           LNFNIVCKRLGAERMSYYLNEAAS
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intron	complement(135046..1351 12)	/locus-tag="An18g01590"
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exon	complement(135113..1352 02)	/locus-tag="An18g01590"
		/number=4
gene	complement(<135940..>13 7166)	/locus-tag="An18g01600"
mRNA	complement(join(<135940 ..136119, 136175..136476, 136534..136864, 136972..>137166))	/locus-tag="An18g01600"
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		/inference="profile:COGS:COG0515" /note="unnamed protein product; Function: srpk2 was first found to mediate the interaction and localization of pre-mRNA splicing factors by phosphorylating the SR (serine/arginine-rich) family of splicing factors and therefore probably controls the activity of splicing. Phenotype: overexpression of srpk2 in M. musculus causes disassembly of cotransfected SF2/ASF and endogenous SC35. Similarity: the ORF shows similarity to several protein kinases from different species and with various specificity. Title: strong similarity to serine/arginine-rich protein-specific kinase srpk2 - Mus musculus deleted EC-number 2.7.1.37" /citation=[41] /codon-start=1 /protein-id="CAK47233.1" /db-xref="GI:134084200" /translation="MASLLKWIRASIHPRRAPLP PRRFPTTGFTIIPASTILEEEHFN SFTNGHYYPVNIGDVFASKYQMIRSHRYVTLKIY TRDESHTEEFKTYQHISQANPSHP GYGYVRTALDTFIIPRPGGDHPCLVQQPMWDSFT DLLFRNPRHRFTEDLLKAGLMQVF LALDYLHTECRVVHTDIKGGNILQEIRDNSLMEA FTAGEMERPSSRKLADGVPVYASR RFGLPISFGRAVLSDFGSAVRGDESRDHDAQPAV YRSPEVMLQVGWSYLVDIWNVGVM IWDLFEGKHMFYGEDPDGKGYSTRAHLAEVIGLL GHPPLDLLQRGKRSHEFFTEDGML S"
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                139790..>140061))
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                                                 sequence:PIR:A40711"
                                                 /note="unnamed protein product;
                                                 Function: srb4 of S. cerevisiae is
                                                 a component of the multi
                                                 subunitcomplex, which binds to RNA
                                                 polymerase II and is essential for
                                                 efficient establishment of the
                                                 transcription initiation
                                                 apparatus. Phenotype: the S.
                                                 cerevisiae srb4 the null mutant is
                                                 inviable and srb4 mutants display
                                                 global defects in mRNA synthesis.
                                                 Remark: an alternate name for srb4
                                                 of S. cerevisiae is YER022w.
                                                 Title: strong similarity to RNA
                                                 polymerase II suppressor protein
                                                 Srb4 - Saccharomyces cerevisiae
                                                 nucleus"
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                                                 LYKRRAEILQFAMQAHMEALFALD
                                                 FVSLLLSKHTPRQAETSMSAFLKQVAPLGSLNAE
                                                 IVEPPPKSEAAVQDVKTVSRGWRA
                                                 QNFNAAANKLLNSATRLEEEVASETKYWDEVLAV
                                                 KEKGWKVCRLPRERTALGVQYGFL
                                                 EATPIFRDRGLAALRRADNGSLILDKGLAPQKTR
                                                 TVRVRVKHRGQLTGCSKMPDPIPD
                                                 AASVERRILQARDTVYEEELFHELMREARIMGSH
                                                 GVTTRQNLVRLPISEDQEILLDLV
                                                 DADRETPDEDKIESTEHDVLANGLSHSIRILLAY
```

```
                                      AHRQNLRRRTQPPPPLSQKRRLTP
                                      EYQLLRPVMAYLQHSSHVRWLESFMNDIYRVLRA
                                      AGIERDFHAVPFASVSLPKVQAVP
                                      KVESLVQQFLMPFESTFSGHLITPQSSFRVKIRT
                                      NPVSPPFGTHYDISIDLPHHPEVQ
                                      PPGRVGLQNEAAAALMHFVKLDIVSAIALQGSKT
                                      TKNTTKKEGAEGTLTWEAAYPHHG
                                      ELLAFSTAGQSKKLKISLSREELKVETFSLRGLE
                                      GFGRSGGPKAPSLQSQTWTATQTD
                                      SKPGLMDFVAEVSREQS"
exon              complement(138020..1392  /locus-tag="An18g01610"
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intron            complement(139288..1393  /locus-tag="An18g01610"
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exon              complement(139338..1397  /locus-tag="An18g01610"
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exon              complement(139790..1400  /locus-tag="An18g01610"
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                                           /number=3
gene              complement(<141613..>14  /locus-tag="An18g01620"
                  3279)
mRNA              complement(join(<141613  /locus-tag="An18g01620"
                  ..142684,
                  142735..>143279))
CDS               complement(join(141613.  /locus-tag="An18g01620"
                  .142684,
                  142735..143279))
                                           /EC-number="5.2.1.5"
                                           /inference="profile:COGS:COG4716"
                                           /note="unnamed protein product;
                                           Catalytic activity: linoleate
                                           isomerases catalyse the
                                           isomerisation of
                                           9-cis,12-cis-octadecadienoate <=>
                                           9-cis,11-trans-octadecadienoate.
                                           Function: linoleate isomerase of
                                           patent WO9932604-A1 is used to
                                           produce conjugated
                                           linoleic/linolenic acid (CLA) from
                                           oils such as sunflower oil,
                                           safflower oil, corn oil, linseed
                                           oil, etc. Similarity: the ORF
                                           shows strong similarity to
                                           myosin-crossreactive antigen,
                                           which could induce autoimmune
                                           reactions in vertebrates. Title:
                                           strong similarity to linoleate
                                           isomerase from patent WO9932604-A1
                                           - Lactobacillus reuteri"
                                           /codon-start=1
                                           /protein-id="CAK47235.1"
                                           /db-xref="GI:134084202"
                                           /translation="MNRGNGLPKRDPKTTQAWLI
                                           GSGISSLAGAVHLIHDAGVPAANI
                                           HILDVHSHAGGGIKSCGDAKSGYVLYTGSLPYFH
                                           DRCVEHLLSLVPSVDDPKQSLLDS
```

```
                                        IKELDRATSPKKSAPTRLIKHGDKGPECLYSKHL
                                        QIGPKYRMELIKLMLENERILGEK
                                        AIQDAFDEAFFKTNFWTLWATTFALQPWHSLVEF
                                        RRCLCKHLAEIERLNDVKALDRTK
                                        YTIYESVIMPIESYLKSQGVDFHFNAKVTNLQIN
                                        PKEAQTTVSGIIIKDNGEQKTIEV
                                        RPEDLVMVTLGSTTSATERGSNDKAPAAPPQHSK
                                        EFLDDDWALWIDLMQASTDYGNPF
                                        NFHNNVDQSTLESFTVTLRDSDFMERYEKLTNNK
                                        PGTGALLSFSDSNWGLSISVPRQP
                                        VCSDQPSSVDVFWGYGLHPEKTGNFVHKPMCHCS
                                        GKEILTEVLSQLGMPVDDMLANSI
                                        TNPVLMPMATAPLMPRRHDYRPEVIPPQSRNLAL
                                        VGQYVEIQDDTTLSMEYSVRGAQM
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exon          complement(141613..1426   /locus-tag="An18g01620"
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intron        complement(142685..1427   /locus-tag="An18g01620"
              34)
                                        /number=1
exon          complement(142735..1432   /locus-tag="An18g01620"
              79)
                                        /number=2
gene          <144032..>145578          /locus-tag="An18g01630"
mRNA          join(<144032..144169,     /locus-tag="An18g01630"
              144230..145373,
              145427..>145578)
CDS           join(144032..144169,      /locus-tag="An18g01630"
              144230..145373,
              145427..145578)
                                        /EC-number="1.5.3.-"
                                        /inference="profile:COGS:COG0277"
                                        /inference="profile:PFAM:PF01565"
                                        /note="unnamed protein product;
                                        Catalytic activity: HDNO of A.
                                        oxidans catalyses
                                        (D)-6-hydroxynicotine + H(2)O +
                                        O(2) =
                                        1-(6-hydroxypyrid-3-yl)-4-(methyla
                                        mino)butan-1-one + H(2)O(2).
                                        Induction: HDNO of A. oxidans
                                        requires FAD in the enzymatic
                                        assay for maximal enzyme activity.
                                        Similarity: the ORF shows
                                        similarity to several
                                        FAD-dependent oxygenases from
                                        different species and with various
                                        specificity. Title: strong
                                        similarity to 6-hydroxy-D-nicotine
                                        oxidase 6-HDNO - Arthrobacter
                                        oxidans"
                                        /citation=[4]
                                        /codon-start=1
                                        /protein-id="CAK47236.1"
                                        /db-xref="GI:134084203"
                                        /translation="MPFLSFARALELRRQLEGTR
                                        AEVVCIGSDDYATSIRRWSDTCEK
                                        EAGAVVRVTSTSEVAEVVRFCRKNHIDFVVEAGG
                                        HSTTGASSSHGGVVISMARMCKVL
                                        TDPASETVCVQGGANWDMVNHSTAPYGLAVVGAT
                                        ASHSGVGGSALGGGFGWLTGQHGL
```

```
                                     IADQLLSVKMVLADGSIVEASDEDNQDLFWAVRG
                                     AGQAFGVATEFVFRAHKVRDRFFG
                                     GLVYYDVDKLPMLVSFANEFDKRQDPKSGFFFGF
                                     AAPREIGHMVVLAVLFYDGSAYDG
                                     EAFFEPILNPNPLINRAAMKSYIEMNSIANVDPV
                                     PEGRKSIGGANIMPPLETSLLQNL
                                     YSQFKEAMNTYPRMEDSALVFELLPYTKAVQVPI
                                     KETACANRGPYYNVGLILCWHDSD
                                     LDAKMHALQRSIISKILEAQRDITDDHAVVYPNL
                                     AGHDVSAEKLFGANLPRLQKLKKK
                                     YDPHNVFRKWHDLLAPARSHVEQTDKP"
exon           144032..144169        /locus-tag="An18g01630"
                                     /number=1
intron         144170..144229        /locus-tag="An18g01630"
                                     /number=1
exon           144230..145373        /locus-tag="An18g01630"
                                     /number=2
intron         145374..145426        /locus-tag="An18g01630"
                                     /number=2
exon           145427..145578        /locus-tag="An18g01630"
                                     /number=3
gene           <146433..>148685      /locus-tag="An18g01640"
mRNA           join(<146433..146489, /locus-tag="An18g01640"
               146546..146952,
               146998..147273,
               147331..147795,
               147845..147954,
               148006..>148685)
CDS            join(146433..146489,  /locus-tag="An18g01640"
               146546..146952,
               146998..147273,
               147331..147795,
               147845..147954,
               148006..148685)
                                     /EC-number="2.4.1.-"
                                     /inference="profile:COGS:COG0438"
                                     /inference="similar to AA
                                     sequence:PIR:T00130"
                                     /note="unnamed protein product;
                                     Function: TSase of G. frondosa
                                     catalyzes the trehalose synthesis
                                     from alpha-D-glucose 1-phosphate
                                     and D-glucose. Similarity: the ORF
                                     shows similarity to a
                                     clock-controlled gene (ccgs) of N.
                                     crassa with unknown function.
                                     Title: strong similarity to
                                     trehalose synthase TSase - Grifola
                                     frondosa"
                                     /citation=[47]
                                     /citation=[49]
                                     /codon-start=1
                                     /protein-id="CAK47237.1"
                                     /db-xref="GI:134084204"
                                     /translation="MSSARSPFDAESWSGKPLNV
                                     IYAGITELVCNNSSGRVAIAIRNL
                                     TDLVDFLVCTWHALRPNVSDYATDTIIAELKDYR
                                     EKNTEKIISAALHQSLVYRCPSLC
                                     SRLWSELDIVPLVLEHKDRERRHDDQGELATFAG
                                     WNKKELDERADSMVRKCIRSFGIG
                                     HVLHNHINFDGSVDVDRGYHVHLANAKDYEKTVD
                                     PATWSMAQCFAQDLREREVKVAFF
```

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                                    SMTCQGKPDVPTRHALSRFTKSLGVRIKWFVPKP
                                    RPGMIPLIRKMQDTLEGQGDPLSD
                                    ITINDELLILDFAYANARRYWLCENGPLRPRAEG
                                    GVDVVIIDSAPLLTLAILSKQQDP
                                    ERPVIFESSLQPQGVSLSGTSSPQSRAWDFIRTR
                                    LTHVDLVVSLLPKELAPRIMPEEN
                                    VGYMSFSVDQLDGQNKPLTDWDVGFYGREFSSLC
                                    RTLQMSIIRYPEEQYILHLSQFRP
                                    GDGTLCLLHSYQKFCDAYTKEHPGRQVPKLLICH
                                    RGPFRTPESTVFYDAAMSQIDSSE
                                    TLSTSVCIIPIGAVDQMWNALLTNARALVQLSTL
                                    HGVPEMLLAAIQKGTPVIAVREAE
                                    LFPFVHESENAILVDKGDEEGIARCFSRIFSVDE
                                    VRQGEGDAGFRKLSDSNTTVGNAV
                                    CWLYLASKMSRGDKFEPRGADIYKLAREEAGYNE
                                    CDWHAV"
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Feature	Location	Qualifiers
exon	146433..146489	/locus-tag="An18g01640" /number=1
intron	146490..146545	/locus-tag="An18g01640" /number=1
exon	146546..146952	/locus-tag="An18g01640" /number=2
intron	146953..146997	/locus-tag="An18g01640" /number=2
exon	146998..147273	/locus-tag="An18g01640" /number=3
intron	147274..147330	/locus-tag="An18g01640" /number=3
exon	147331..147795	/locus-tag="An18g01640" /number=4
intron	147796..147844	/locus-tag="An18g01640" /number=4
exon	147845..147954	/locus-tag="An18g01640" /number=5
intron	147955..148005	/locus-tag="An18g01640" /number=5
exon	148006..148685	/locus-tag="An18g01640" /number=6
gene	complement(149158..1492 30)	/gene="tRNA-Lys (CTT)" /locus-tag="An18e01650"
tRNA	complement(149158..1492 30)	/gene="tRNA-Lys (CTT)" /locus-tag="An18e01650" /product="tRNA-Lys" /inference="profile:tRNAscan:1.4" /note="codon recognized: AAG"
gene	<149921..>150603	/locus-tag="An18g01660"
mRNA	join(<149921..149936, 150144..150502, 150577..>150603)	/locus-tag="An18g01660"
CDS	join(149921..149936, 150144..150502, 150577..150603)	/locus-tag="An18g01660" /note="unnamed protein product; Remark: the ORF is questionable due to its suboptimal intron-exon structure. Similarity: the ORF overlaps with the 5' region of the A. niger pfkA gene. Title: questionable ORF" /codon-start=1

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                                                        /protein-id="CAK47238.1"
                                                        /db-xref="GI:134084205"
                                                        /translation="MKETESGDIRCFQDCKRKWA
                                                        EEDIPCQHPSRICPLQRAARSPGR
                                                        SAFDEHLALSPADQLSPQWWAVYSVQSTFPSNER
                                                        GYLYSGAVTAGVSDVLVAHTRFFS
                                                        PAPALLFSPTLQTQVISAFPPQALLLIPNNC"
exon              149921..149936                        /locus-tag="An18g01660"
                                                        /number=1
intron            149937..150143                        /locus-tag="An18g01660"
                                                        /number=1
exon              150144..150502                        /locus-tag="An18g01660"
                                                        /number=2
intron            150503..150576                        /locus-tag="An18g01660"
                                                        /number=2
exon              150577..150603                        /locus-tag="An18g01660"
                                                        /number=3
gene              <150631..>153085                      /gene="pfkA"
                                                        /locus-tag="An18g01670"
mRNA              join(<150631..151371,                 /gene="pfkA"
                  151428..151889,
                  151937..>153085)
                                                        /locus-tag="An18g01670"
CDS               join(150631..151371,                  /gene="pfkA"
                  151428..151889,
                  151937..153085)
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                                                        /inference="profile:COGS:COG0205"
                                                        /inference="profile:PFAM:PF00365"
                                                        /inference="similar to AA
                                                        sequence:SWISSPROT:K6PF.ASPNG"
                                                        /note="Catalytic activity: pfkA of
                                                        A. niger is catalysing ATP +
                                                        D-fructose 6-phosphate <=> ADP +
                                                        D-fructose 1,6-bisphosphate.
                                                        Function: pfkA of A. niger is
                                                        active in a key control step of
                                                        glycolysis. Gene-ID: pfkA
                                                        Similarity: the ORF overlaps with
                                                        the sequence of entry EMBL:ANPFKA
                                                        (A. niger pfkA gene) cytoplasm"
                                                        /citation=[1]
                                                        /citation=[5]
                                                        /citation=[21]
                                                        /citation=[35]
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                                                        /product="6-phosphofructokinase
                                                        pfkA-Aspergillus niger"
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                                                        /db-xref="GI:134084206"
                                                        /db-xref="InterPro:IPR000023"
                                                        /db-xref="InterPro:IPR009161"
                                                        /translation="MAPPQAPVQPPKRRRIGVLT
                                                        SGGDAPGMNGVVRAVVRMAIHSDC
                                                        EAFAVYEGYEGLVNGGDMIRQLHWEDVRGWLSRG
                                                        GTLIGSARCMTFRERPGRLRAAKN
                                                        MVLRGIDALVVCGGDGSLTGADVFRSEWPGLLKE
                                                        LVETGELTEEQVKPYQILNIVGLV
                                                        GSIDNDMSGTDATIGCYSSLTRICDAVDDVFDTA
                                                        FSHQRGFVIEVMGRHCGWLALMSA
                                                        ISTGADWLFVPEMPPKDGWEDDMCAIITKNRKER
```

```
                                         GKRRTIVIVAEGAQDRHLNKISSS
                                         KIKDILTERLNLDTRVTVLGHTQRGGAACAYDRW
                                         LSTLQGVEAVRAVLDMKPEAPSPV
                                         ITIRENKILRMPLMDAVQHTKTVTKHIQNKEFAE
                                         AMALRDSEFKEYHFSYINTSTPDH
                                         PKLLLPENKRMRIGIIHVGAPAGGMNQATRAAVA
                                         YCLTRGHTPLAIHNGFPGLCRHYD
                                         DTPICSVREVAWQESDAWVNEGGSDIGTNRGLPG
                                         DDLATTAKSFKKFGFDALFVVGGF
                                         EAFTAVSQLRQAREKYPEFKIPMTVLPATISNNV
                                         PGTEYSLGSDTCLNTLIDFCDAIR
                                         QSASSSRRRVFVIETQGGKSGYIATTAGLSVGAV
                                         AVYIPEEGIDIKMLARDIDFLRDN
                                         FARDKGANRAGKIILRNECASSTYTTQVVADMIK
                                         EEAKGRFESRAAVPGHFQQGGKPS
                                         PMDRIRALRMATKCMLHLESYAGKSADEIAADEL
                                         SASVIGIKGSQVLFSPMGGETGLE
                                         ATETDWARRRPKTEFWLELQDTVNILSGRASVNN
                                         ATWSCYENA"
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                                         /number=1
exon            151428..151889           /gene="pfkA"
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                                         /number=2
intron          151890..151936           /gene="pfkA"
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                                         /number=2
exon            151937..153085           /gene="pfkA"
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gene            complement(<153410..>15  /locus-tag="An18g01680"
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mRNA            complement(join(<153410  /locus-tag="An18g01680"
                ..153429,
                153509..>154508))
CDS             complement(join(153410.  /locus-tag="An18g01680"
                .153429,
                153509..154508))
                                         /EC-number="1.6.-.-"
                                         /inference="profile:COGS:COG0492"
                                         /inference="profile:PFAM:PF00070"
                                         /inference="similar to AA
                                         sequence:UniProtKB:AF281147.1"
                                         /note="unnamed protein product;
                                         Catalytic activity: NADH
                                         dehydrogenases catalyse NADH +
                                         acceptor <=> NAD(+) + reduced
                                         acceptor. Function: ndh of P.
                                         fluorescens is involved in
                                         colonization of this bacterium.
                                         Phenotype: in an oxygen-poor
                                         medium mutant PCL1201 of P.
                                         fluorescens, which carries a
                                         mutation in the ndh gene showed a
                                         decreased growth rate. Remark: the
                                         sequence of the database entry
                                         EMBL:ANPFKA (A. niger pfkA gene)
                                         overlaps with the ORF due a
```

```
                                      probably wrong nummer of 4658 bp
                                      for the coding sequence of the A.
                                      niger protein, which is encoded
                                      3'. Similarity: the ORF is 112
                                      amino acids shorter at its
                                      C-terminal end than ndh of P.
                                      fluorescens. Title: similarity to
                                      NADH dehydrogenase II ndh
                                      -Pseudomonas fluorescens
                                      localisation:mitochondrion"
                                      /citation=[46]
                                      /codon-start=1
                                      /protein-id="CAK47240.1"
                                      /db-xref="GI:134084207"
                                      /translation="MTTDKTITIPIIGASFAGLT
                                      TAHSLLSHFTTNKSKGIKIKILLI
                                      NPTPNFYWAIAAPRILAKPTAFSESQYLIPIADG
                                      FTKYSPEVFEFILGRATSLDFENK
                                      LLQVEESTTNNTNKALREIKYDYLVIASGSTPSA
                                      SSSSPLFPGETETENKDADRKEVI
                                      YPFKLSPTSTSTITETIQSAQHTISTSKKITIIG
                                      AGPIGVELAGELADLTSSASSKEK
                                      KDITLISSTPRILPVLKESASGTATSLLTSKGVR
                                      VLTNTKVISVSASKEGGGGYELKF
                                      ENGETMDTDIYIPTIGVLPNSSYIPGEVLDEKGW
                                      VRVDSELKVVGVDGVYAAGDVTDL LGRGG"
sig-peptide       complement(154443..1545 /locus-tag="An18g01680"
                  08)
                                      /inference="protein
                                      motif:SignalP:2.0"
mat-peptide       complement(join(153413. /locus-tag="An18g01680"
                  .153429,
                  153509..154442))
                                      /product="unnamed"
exon              complement(153410..1534 /locus-tag="An18g01680"
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                                      /number=1
intron            complement(153430..1535 /locus-tag="An18g01680"
                  08)
                                      /number=1
exon              complement(153509..1545 /locus-tag="An18g01680"
                  08)
                                      /number=2
gene              complement(<154789..>15 /locus-tag="An18g01690"
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mRNA              complement(join(<154789 /locus-tag="An18g01690"
                  ..154869,
                  154921..155060,
                  155120..155914,
                  155981..156128,
                  156179..156193,
                  156245..156318,
                  156371..>156395))
CDS               complement(join(154789. /locus-tag="An18g01690"
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                  155120..155914,
                  155981..156128,
                  156179..156193,
                  156245..156318,
                  156371..156395))
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                                      sequence:PIR:S67043"
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                                     Title: strong similarity to
                                     hypothetical protein YOR155c –
                                     Saccharomyces cerevisiae"
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                                     FVLHSQPTAVYQEHSENLIAVAADTHQRYAEIFR
                                     DVEMLIRDHITHQQDDAPGKSKLK
                                     LLVPTVGTFFTPLYLVDAFRRQDAQRFISRRRFV
                                     APSFNDIRLILNSAQLIGLARTTG
                                     VDLVTFDGDVTLYDDGACLTDDNPVILRIMRLLL
                                     QGRKVGIVTAAGYTDAAKYYERLK
                                     GLLDAMYESAEMTDAQRAGLVVMGGESNFLFRYD
                                     HASPSRLSYVPREEWLLEEMKTWQ
                                     EGDITRLLDIAESSLRACASNLNLPVAVLRKDRA
                                     VGVYPTERGRISREQLEETVLVVQ
                                     NTVERSEVGARLPFCAFNGGNDVFVDIGDKSWGV
                                     RACQRYFGGIEPARTLHVGDQFLS
                                     AGANDFKARLASTTAWIASPAETVQLLDELQGI"
exon              complement(154789..1548  /locus-tag="An18g01690"
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                                     /number=2
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intron            complement(155915..1559  /locus-tag="An18g01690"
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exon              complement(155981..1561  /locus-tag="An18g01690"
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                  78)
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intron            complement(156319..1563  /locus-tag="An18g01690"
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exon              complement(156371..1563  /locus-tag="An18g01690"
                  95)
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gene              complement(<156827..>15  /locus-tag="An18g01700"
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                     8638)
mRNA                 complement(join(<156827    /locus-tag="An18g01700"
                     ..157888,
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                     158115..158310,
                     158364..>158638))
CDS                  complement(join(156827.    /locus-tag="An18g01700"
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                     158115..158310,
                     158364..158638))
                                                /inference="profile:COGS:COG0477"
                                                /inference="profile:PFAM:PF00083"
                                                /note="unnamed protein product;
                                                Function: qutD of E. nidulans is
                                                involved in quinic acid transport
                                                with similarity to the maltose
                                                transport protein MAL61.
                                                Phenotype: mutations in the qutD
                                                gene of A. nidulans cause the loss
                                                of ability to grow upon quinic
                                                acid as sole carbon source in
                                                media at normal pH 6. 5 and
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seven different mutant alleles of
CaMDR1 from C. albicans showed
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162301 acaaggtcca gaaagactac ctccatggta ttagcacaag acaatcgtat gatcagctca
162361 tccaattcct tgtagctaca ccagagaaat taatgtggtg aagtgatact gacagtatct
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CAS REGISTRY NO. (RN):    928583-76-0
SEQUENCE LENGTH (SQL):    226503
MOLECULE TYPE (CI):       DNA; linear
DIVISION CODE (CI):       Plants, fungi, algae
DATE (DATE):              24 Mar 2007
DEFINITION (DEF):         Aspergillus niger contig An14c0180, complete genome.
SOURCE:                   Aspergillus niger
 ORGANISM (ORGN):         Aspergillus niger
                          Eukaryota; Fungi; Ascomycota; Pezizomycotina;
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                          Trichocomaceae; Aspergillus
REFERENCE:                1  (bases 23835 to 25756)
   AUTHOR (AU):           Jones,S.W.; Luk,K.C.
   TITLE (TI):            Isolation of a chicken thioredoxin cDNA clone.
                          Thioredoxin mRNA is differentially expressed in normal
                          and Rous sarcoma virus-transformed chicken embryo
                          fibroblasts
   JOURNAL (SO):          J. Biol. Chem., 263 (20), 9607-9611 (1988)
   OTHER SOURCE (OS):     CA 109:105752
REFERENCE:                2  (bases 16557 to 19301)
   AUTHOR (AU):           Robinson,J.S.; Klionsky,D.J.; Banta,L.M.; Emr,S.D.
   TITLE (TI):            Protein sorting in Saccharomyces cerevisiae: isolation
                          of mutants defective in the delivery and processing of
                          multiple vacuolar hydrolases
   JOURNAL (SO):          Mol. Cell. Biol., 8 (11), 4936-4948 (1988)
   OTHER SOURCE (OS):     CA 110:20954
REFERENCE:                3  (bases 181479 to 182990)
   AUTHOR (AU):           Jackson,B.J.; Warren,C.D.; Bugge,B.; Robbins,P.W.
   TITLE (TI):            Synthesis of lipid-linked oligosaccharides in
                          Saccharomyces cerevisiae: Man2GlcNAc2 and Man1GlcNAc2
                          are transferred from dolichol to protein in vivo
   JOURNAL (SO):          Arch. Biochem. Biophys., 272 (1), 203-209 (1989)
   OTHER SOURCE (OS):     CA 111:74550
REFERENCE:                4  (bases 197258 to 198879)
   AUTHOR (AU):           Szumanski,M.B.; Boyle,S.M.
   TITLE (TI):            Analysis and sequence of the speB gene encoding
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                                 agmatine ureohydrolase, a putrescine biosynthetic
                                 enzyme in Escherichia coli
        JOURNAL (SO):            J. Bacteriol., 172 (2), 538-547 (1990)
        OTHER SOURCE (OS):       CA 113:18542
    REFERENCE:                   5   (bases 8900 to 10226)
        AUTHOR (AU):             Lambert,S.; Yu,H.; Prchal,J.T.; Lawler,J.; Ruff,P.;
                                 Speicher,D.; Cheung,M.C.; Kan,Y.W.; Palek,J.
        TITLE (TI):              cDNA sequence for human erythrocyte ankyrin
        JOURNAL (SO):            Proc. Natl. Acad. Sci. U.S.A., 87 (5), 1730-1734 (1990)
        OTHER SOURCE (OS):       CA 113:146283
    REFERENCE:                   6   (bases 149275 to 150765)
        AUTHOR (AU):             Chen,W.N.; Balzi,E.; Capieaux,E.; Choder,M.; Goffeau,A.
        TITLE (TI):              The DNA sequencing of the 17 kb HindIII fragment
                                 spanning the LEU1 and ATE1 loci on chromosome VII from
                                 Saccharomyces cerevisiae reveals the PDR6 gene, a new
                                 member of the genetic network controlling pleiotropic
                                 drug resistance
        JOURNAL (SO):            Yeast, 7 (3), 287-299 (1991)
        OTHER SOURCE (OS):       CA 116:16482
    REFERENCE:                   7   (bases 20272 to 22263)
        AUTHOR (AU):             Tobias,J.W.; Varshavsky,A.
        TITLE (TI):              Cloning and functional analysis of the
                                 ubiquitin-specific protease gene UBP1 of Saccharomyces
                                 cerevisiae
        JOURNAL (SO):            J. Biol. Chem., 266 (18), 12021-12028 (1991)
        OTHER SOURCE (OS):       CA 116:122304
    REFERENCE:                   8   (bases 92137 to 93393)
        AUTHOR (AU):             Gosalbes,M.J.; Perez-Gonzalez,J.A.; Gonzalez,R.;
                                 Navarro,A.
        TITLE (TI):              Two beta-glycanase genes are clustered in Bacillus
                                 polymyxa: molecular cloning, expression, and sequence
                                 analysis of genes encoding a xylanase and an
                                 endo-beta-(1,3)-(1,4)-glucanase
        JOURNAL (SO):            J. Bacteriol., 173 (23), 7705-7710 (1991)
        OTHER SOURCE (OS):       CA 118:33731
    REFERENCE:                   9   (bases 159715 to 163074)
        AUTHOR (AU):             Kumar,V.; Ramakrishnan,S.; Teeri,T.T.; Knowles,J.K.;
                                 Hartley,B.S.
        TITLE (TI):              Saccharomyces cerevisiae cells secreting an Aspergillus
                                 niger beta-galactosidase grow on whey permeate
        JOURNAL (SO):            Biotechnology (N.Y.), 10 (1), 82-85 (1992)
    REFERENCE:                   10 (bases 197258 to 198879)
        AUTHOR (AU):             Szumanski,M.B.; Boyle,S.M.
        TITLE (TI):              Influence of cyclic AMP, agmatine, and a novel protein
                                 encoded by a flanking gene on speB (agmatine
                                 ureohydrolase) in Escherichia coli
        JOURNAL (SO):            J. Bacteriol., 174 (3), 758-764 (1992)
        OTHER SOURCE (OS):       CA 119:21634
    REFERENCE:                   11 (bases 16557 to 19301)
        AUTHOR (AU):             Wada,Y.; Ohsumi,Y.; Anraku,Y.
        TITLE (TI):              Genes for directing vacuolar morphogenesis in
                                 Saccharomyces cerevisiae. I. Isolation and
                                 characterization of two classes of vam mutants
        JOURNAL (SO):            J. Biol. Chem., 267 (26), 18665-18670 (1992)
        OTHER SOURCE (OS):       CA 117:105596
    REFERENCE:                   12 (bases 20272 to 22263)
        AUTHOR (AU):             Baker,R.T.; Tobias,J.W.; Varshavsky,A.
        TITLE (TI):              Ubiquitin-specific proteases of Saccharomyces
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                                 analysis of the UBP gene family
        JOURNAL (SO):            J. Biol. Chem., 267 (32), 23364-23375 (1992)
        OTHER SOURCE (OS):       CA 119:23561
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REFERENCE:               13 (bases 16557 to 19301)
   AUTHOR (AU):          Horazdovsky,B.F.; Emr,S.D.
   TITLE (TI):           The VPS16 gene product associates with a
                         sedimentable protein complex and is essential for
                         vacuolar protein sorting in yeast
   JOURNAL (SO):         J. Biol. Chem., 268 (7), 4953-4962 (1993)
   OTHER SOURCE (OS):    CA 118:229898
REFERENCE:               14 (bases 32776 to 34762)
   AUTHOR (AU):          Roebroek,A.J.; Creemers,J.W.; Pauli,I.G.; Bogaert,T.;
                         Van de Ven,W.J.
   TITLE (TI):           Generation of structural and functional diversity in
                         furin-like proteins in Drosophila melanogaster by
                         alternative splicing of the Dfur1 gene
   JOURNAL (SO):         EMBO J., 12 (5), 1853-1870 (1993)
   OTHER SOURCE (OS):    CA 120:70454
REFERENCE:               15 (bases 181479 to 182990)
   AUTHOR (AU):          Jackson,B.J.; Kukuruzinska,M.A.; Robbins,P.
   TITLE (TI):           Biosynthesis of asparagine-linked oligosaccharides in
                         Saccharomyces cerevisiae: the alg2 mutation
   JOURNAL (SO):         Glycobiology, 3 (4), 357-364 (1993)
   OTHER SOURCE (OS):    CA 120:126513
REFERENCE:               16 (bases 22652 to 23365)
   AUTHOR (AU):          Errabolu,R.; Sanders,M.A.; Salisbury,J.L.
   TITLE (TI):           Cloning of a cDNA encoding human centrin, an EF-hand
                         protein of centrosomes and mitotic spindle poles
   JOURNAL (SO):         J. Cell. Sci., 107 (PT 1), 9-16 (1994)
   OTHER SOURCE (OS):    CA 122:3785
REFERENCE:               17 (bases 72683 to 73072)
   AUTHOR (AU):          Ishikawa,A.; Ohta,S.; Matsuoka,K.; Hattori,T.;
                         Nakamura,K.
   TITLE (TI):           A family of potato genes that encode Kunitz-type
                         proteinase inhibitors: structural comparisons and
                         differential expression
   JOURNAL (SO):         Plant Cell Physiol., 35 (2), 303-312 (1994)
   OTHER SOURCE (OS):    CA 121:100855
REFERENCE:               18 (bases 149275 to 150765)
   AUTHOR (AU):          Lai,M.H.; Bard,M.; Pierson,C.A.; Alexander,J.F.;
                         Goebl,M.; Carter,G.T.; Kirsch,D.R.
   TITLE (TI):           The identification of a gene family in the
                         Saccharomyces cerevisiae ergosterol biosynthesis
                         pathway
   JOURNAL (SO):         Gene, 140 (1), 41-49 (1994)
   OTHER SOURCE (OS):    CA 121:127004
REFERENCE:               19 (bases 176803 to 178484)
   AUTHOR (AU):          Kil,K.S.; Cunningham,M.W.; Barnett,L.A.
   TITLE (TI):           Cloning and sequence analysis of a gene encoding a
                         67-kilodalton myosin-cross-reactive antigen of
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   JOURNAL (SO):         Infect. Immun., 62 (6), 2440-2449 (1994)
   OTHER SOURCE (OS):    CA 122:73390
REFERENCE:               20 (bases 48251 to 50618)
   AUTHOR (AU):          Sato,S.; Suzuki,H.; Widyastuti,U.; Hotta,Y.; Tabata,S.
   TITLE (TI):           Identification and characterization of genes induced
                         during sexual differentiation in Schizosaccharomyces
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   JOURNAL (SO):         Curr. Genet., 26 (1), 31-37 (1994)
   OTHER SOURCE (OS):    CA 121:197248
REFERENCE:               21 (bases 157327 to 158616)
   AUTHOR (AU):          Marcus,G.A.; Silverman,N.; Berger,S.L.; Horiuchi,J.;
                         Guarente,L.
   TITLE (TI):           Functional similarity and physical association between
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                            GCN5 and ADA2: putative transcriptional adaptors
     JOURNAL (SO):   EMBO J., 13 (20), 4807-4815 (1994)
     OTHER SOURCE (OS):   CA 122:2700
  REFERENCE: 22 (bases 149275 to 150765)
     AUTHOR (AU):   Lees,N.D.; Skaggs,B.; Kirsch,D.R.; Bard,M.
     TITLE (TI):   Cloning of the late genes in the ergosterol
                           biosynthetic pathway of Saccharomyces cerevisiae--a
                           review
     JOURNAL (SO):   Lipids, 30 (3), 221-226 (1995)
     OTHER SOURCE (OS):   CA 123:79105
  REFERENCE: 23 (bases 157327 to 158616)
     AUTHOR (AU):   Horiuchi,J.; Silverman,N.; Marcus,G.A.; Guarente,L.
     TITLE (TI):   ADA3, a putative transcriptional adaptor, consists of
                           two separable domains and interacts with ADA2 and GCN5
                           in a trimeric complex
     JOURNAL (SO):   Mol. Cell. Biol., 15 (3), 1203-1209 (1995)
     OTHER SOURCE (OS):   CA 122:232629
  REFERENCE: 24 (bases 41237 to 43709)
     AUTHOR (AU):   Harris,C.L.; Kolanko,C.J.
     TITLE (TI):   Aminoacyl-tRNA synthetase complex in Saccharomyces
                           cerevisiae
     JOURNAL (SO):   Biochem. J., 309 (PT 1), 321-324 (1995)
     OTHER SOURCE (OS):   CA 123:106013
  REFERENCE: 25 (bases 190148 to 191691)
     AUTHOR (AU):   Russo,M.W.; Sevetson,B.R.; Milbrandt,J.
     TITLE (TI):   Identification of NAB1, a repressor of NGFI-A- and
                           Krox20-mediated transcription
     JOURNAL (SO):   Proc. Natl. Acad. Sci. U.S.A., 92 (15), 6873-6877
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     OTHER SOURCE (OS):   CA 123:277433
  REFERENCE: 26 (bases 163244 to 165037)
     AUTHOR (AU):   Saupe,S.; Turcq,B.; Begueret,J.
     TITLE (TI):   A gene responsible for vegetative incompatibility in
                           the fungus Podospora anserina encodes a protein with a
                           GTP-binding motif and G beta homologous domain
     JOURNAL (SO):   Gene, 162 (1), 135-139 (1995)
     OTHER SOURCE (OS):   CA 123:331620
  REFERENCE: 27 (bases 20272 to 22263)
     AUTHOR (AU):   Hochstrasser,M.
     TITLE (TI):   Ubiquitin-dependent protein degradation
     JOURNAL (SO):   Annu. Rev. Genet., 30, 405-439 (1996)
     OTHER SOURCE (OS):   CA 126:43976
  REFERENCE: 28 (bases 65395 to 67116)
     AUTHOR (AU):   Stearman,R.; Yuan,D.S.; Yamaguchi-Iwai,Y.;
                           Klausner,R.D.; Dancis,A.
     TITLE (TI):   A permease-oxidase complex involved in high-affinity
                           iron uptake in yeast
     JOURNAL (SO):   Science, 271 (5255), 1552-1557 (1996)
     OTHER SOURCE (OS):   CA 124:225984
  REFERENCE: 29 (bases 157327 to 158616)
     AUTHOR (AU):   Wolffe,A.P.; Pruss,D.
     TITLE (TI):   Targeting chromatin disruption: Transcription
                           regulators that acetylate histones
     JOURNAL (SO):   Cell, 84 (6), 817-819 (1996)
     OTHER SOURCE (OS):   CA 124:251873
  REFERENCE: 30 (bases 190148 to 191691)
     AUTHOR (AU):   Svaren,J.; Sevetson,B.R.; Apel,E.D.; Zimonjic,D.B.;
                           Milbrandt,J.
     TITLE (TI):   NAB2, a corepressor of NGFI-A (Egr-1) and Krox20, is
                           induced by proliferative and differentiative stimuli
     JOURNAL (SO):   Mol. Cell. Biol., 16 (7), 3545-3553 (1996)
     OTHER SOURCE (OS):   CA 125:106429

REFERENCE: 31 (bases 157327 to 158616)
   AUTHOR (AU):   Kuo,M.H.; Brownell,J.E.; Sobel,R.E.; Ranalli,T.A.;
                        Cook,R.G.; Edmondson,D.G.; Roth,S.Y.; Allis,C.D.
   TITLE (TI):   Transcription-linked acetylation by Gcn5p of histones
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   JOURNAL (SO):   Nature, 383 (6597), 269-272 (1996)
   OTHER SOURCE (OS):   CA 125:268960
REFERENCE: 32 (bases 137703 to 138530)
   AUTHOR (AU):   Bang,D.D.; Ketting,R.; de Ruijter,M.; Brandsma,J.A.;
                        Verhage,R.A.; van de Putte,P.; Brouwer,J.
   TITLE (TI):   Cloning of Schizosaccharomyces pombe rph16+, a gene
                        homologous to the Saccharomyces cerevisiae RAD16 gene
   JOURNAL (SO):   Mutat. Res., 364 (2), 57-71 (1996)
   OTHER SOURCE (OS):   CA 125:294310
REFERENCE: 33 (bases 2852 to 4742)
   AUTHOR (AU):   Murone,M.; Simanis,V.
   TITLE (TI):   The fission yeast dma1 gene is a component of the
                        spindle assembly checkpoint, required to prevent septum
                        formation and premature exit from mitosis if spindle
                        function is compromised
   JOURNAL (SO):   EMBO J., 15 (23), 6605-6616 (1996)
   OTHER SOURCE (OS):   CA 126:208115
REFERENCE: 34 (bases 157327 to 158616)
   AUTHOR (AU):   Chiang,Y.C.; Komarnitsky,P.; Chase,D.; Denis,C.L.
   TITLE (TI):   ADR1 activation domains contact the histone
                        acetyltransferase GCN5 and the core transcriptional
                        factor TFIIB
   JOURNAL (SO):   J. Biol. Chem., 271 (50), 32359-32365 (1996)
   OTHER SOURCE (OS):   CA 126:128325
REFERENCE: 35 (bases 98558 to 100377)
   AUTHOR (AU):   Stukey,J.; Carman,G.M.
   TITLE (TI):   Identification of a novel phosphatase sequence motif
   JOURNAL (SO):   Protein Sci., 6 (2), 469-472 (1997)
   OTHER SOURCE (OS):   CA 126:289905
REFERENCE: 36 (bases 51277 to 53277)
   AUTHOR (AU):   Portman,D.S.; O'Connor,J.P.; Dreyfuss,G.
   TITLE (TI):   YRA1, an essential Saccharomyces cerevisiae gene,
                        encodes a novel nuclear protein with RNA annealing
                        activity
   JOURNAL (SO):   RNA, 3 (5), 527-537 (1997)
   OTHER SOURCE (OS):   CA 127:13954
REFERENCE: 37 (bases 65395 to 67116)
   AUTHOR (AU):   de Silva,D.; Davis-Kaplan,S.; Fergestad,J.; Kaplan,J.
   TITLE (TI):   Purification and characterization of Fet3 protein, a
                        yeast homologue of ceruloplasmin
   JOURNAL (SO):   J. Biol. Chem., 272 (22), 14208-14213 (1997)
   OTHER SOURCE (OS):   CA 127:77719
REFERENCE: 38 (bases 98558 to 100377)
   AUTHOR (AU):   Qie,L.; Nagiec,M.M.; Baltisberger,J.A.; Lester,R.L.;
                        Dickson,R.C.
   TITLE (TI):   Identification of a Saccharomyces gene, LCB3, necessary
                        for incorporation of exogenous long chain bases into
                        sphingolipids
   JOURNAL (SO):   J. Biol. Chem., 272 (26), 16110-16117 (1997)
   OTHER SOURCE (OS):   CA 127:146248
REFERENCE: 39 (bases 19354 to 19996)
   AUTHOR (AU):   Lussier,M.; White,A.M.; Sheraton,J.; di Paolo,T.;
                        Treadwell,J.; Southard,S.B.; Horenstein,C.I.;
                        Chen-Weiner,J.; Ram,A.F.; Kapteyn,J.C.; Roemer,T.W.;
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   TITLE (TI):   Large scale identification of genes involved in cell

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                              cerevisiae
     JOURNAL (SO):   Genetics, 147 (2), 435-450 (1997)
     OTHER SOURCE (OS):   CA 127:327291
REFERENCE: 40 (bases 65395 to 67116)
     AUTHOR (AU):   Yuan,D.S.; Dancis,A.; Klausner,R.D.
     TITLE (TI):   Restriction of copper export in Saccharomyces
                              cerevisiae to a late Golgi or post-Golgi compartment in
                              the secretory pathway
     JOURNAL (SO):   J. Biol. Chem., 272 (41), 25787-25793 (1997)
     OTHER SOURCE (OS):   CA 127:343694
REFERENCE: 41 (bases 183872 to 189440)
     AUTHOR (AU):   Wood,K.W.; Sakowicz,R.; Goldstein,L.S.; Cleveland,D.W.
     TITLE (TI):   CENP-E is a plus end-directed kinetochore motor
                              required for metaphase chromosome alignment
     JOURNAL (SO):   Cell, 91 (3), 357-366 (1997)
     OTHER SOURCE (OS):   CA 128:45048
REFERENCE: 42 (bases 16557 to 19301)
     AUTHOR (AU):   Rieder,S.E.; Emr,S.D.
     TITLE (TI):   A novel RING finger protein complex essential for a
                              late step in protein transport to the yeast vacuole
     JOURNAL (SO):   Mol. Biol. Cell, 8 (11), 2307-2327 (1997)
     OTHER SOURCE (OS):   CA 128:32213
REFERENCE: 43 (bases 218542 to 219708)
     AUTHOR (AU):   Nakamura,T.; Ohmoto,T.; Hirata,D.; Tsuchiya,E.;
                              Miyakawa,T.
     TITLE (TI):   Yeast Crv4/Ttp1, a predicted type II membrane protein,
                              is involved in an event important for growth,
                              functionally overlapping with the event regulated by
                              calcineurin- and Mpk1-mediated pathways
     JOURNAL (SO):   Mol. Gen. Genet., 256 (5), 481-487 (1997)
     OTHER SOURCE (OS):   CA 128:138463
REFERENCE: 44 (bases 163244 to 165037)
     AUTHOR (AU):   Espagne,E.; Balhadere,P.; Begueret,J.; Turcq,B.
     TITLE (TI):   Reactivity in vegetative incompatibility of the HET-E
                              protein of the fungus Podospora anserina is dependent
                              on GTP-binding activity and a WD40 repeated domain
     JOURNAL (SO):   Mol. Gen. Genet., 256 (6), 620-627 (1997)
     OTHER SOURCE (OS):   CA 128:214667
REFERENCE: 45 (bases 98558 to 100377)
     AUTHOR (AU):   Mao,C.; Wadleigh,M.; Jenkins,G.M.; Hannun,Y.A.;
                              Obeid,L.M.
     TITLE (TI):   Identification and characterization of Saccharomyces
                              cerevisiae dihydrosphingosine-1-phosphate phosphatase
     JOURNAL (SO):   J. Biol. Chem., 272 (45), 28690-28694 (1997)
     OTHER SOURCE (OS):   CA 128:72216
REFERENCE: 46 (bases 103137 to 103945)
     AUTHOR (AU):   Kondoh,O.; Tachibana,Y.; Ohya,Y.; Arisawa,M.;
                              Watanabe,T.
     TITLE (TI):   Cloning of the RHO1 gene from Candida albicans and its
                              regulation of beta-1,3-glucan synthesis
     JOURNAL (SO):   J. Bacteriol., 179 (24), 7734-7741 (1997)
     OTHER SOURCE (OS):   CA 128:111391
REFERENCE: 47 (bases 67552 to 68735)
     AUTHOR (AU):   Gonzalez,F.J.; Montes,J.; Martin,F.; Lopez,M.C.;
                              Ferminan,E.; Catalan,J.; Galan,M.A.; Dominguez,A.
     TITLE (TI):   Molecular cloning of TvDAO1, a gene encoding a D-amino
                              acid oxidase from Trigonopsis variabilis and its
                              expression in Saccharomyces cerevisiae and
                              Kluyveromyces lactis
     JOURNAL (SO):   Yeast, 13 (15), 1399-1408 (1997)
     OTHER SOURCE (OS):   CA 128:150109

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REFERENCE:              48 (bases 41237 to 43709)
   AUTHOR (AU):         Motorin,Y.; Le Caer,J.P.; Waller,J.P.
   TITLE (TI):          Cysteinyl-tRNA synthetase from Saccharomyces
                        cerevisiae. Purification, characterization and
                        assignment to the genomic sequence YNL247w
   JOURNAL (SO):        Biochimie, 79 (12), 731-740 (1997)
   OTHER SOURCE (OS):   CA 129:24853
REFERENCE:              49 (bases 98558 to 100377)
   AUTHOR (AU):         Mandala,S.M.; Thornton,R.; Tu,Z.; Kurtz,M.B.;
                        Nickels,J.; Broach,J.; Menzeleev,R.; Spiegel,S.
   TITLE (TI):          Sphingoid base 1-phosphate phosphatase: a key regulator
                        of sphingolipid metabolism and stress response
   JOURNAL (SO):        Proc. Natl. Acad. Sci. U.S.A., 95 (1), 150-155 (1998)
   OTHER SOURCE (OS):   CA 128:151503
REFERENCE:              50 (bases 65395 to 67116)
   AUTHOR (AU):         Gaxiola,R.A.; Yuan,D.S.; Klausner,R.D.; Fink,G.R.
   TITLE (TI):          The yeast CLC chloride channel functions in cation
                        homeostasis
   JOURNAL (SO):        Proc. Natl. Acad. Sci. U.S.A., 95 (7), 4046-4050 (1998)
   OTHER SOURCE (OS):   CA 128:319139
REFERENCE:              51 (bases 151141 to 153445)
   AUTHOR (AU):         Cazelle,B.; Pokorska,A.; Hull,E.; Green,P.M.;
                        Stanway,G.; Scazzocchio,C.
   TITLE (TI):          Sequence, exon-intron organization, transcription and
                        mutational analysis of prnA, the gene encoding the
                        transcriptional activator of the prn gene cluster in
                        Aspergillus nidulans
   JOURNAL (SO):        Mol. Microbiol., 28 (2), 355-370 (1998)
   OTHER SOURCE (OS):   CA 129:63816
REFERENCE:              52 (bases 48251 to 50618)
   AUTHOR (AU):         Lubkowitz,M.A.; Barnes,D.; Breslav,M.; Burchfield,A.;
                        Naider,F.; Becker,J.M.
   TITLE (TI):          Schizosaccharomyces pombe isp4 encodes a transporter
                        representing a novel family of oligopeptide
                        transporters
   JOURNAL (SO):        Mol. Microbiol., 28 (4), 729-741 (1998)
   OTHER SOURCE (OS):   CA 129:119284
REFERENCE:              53 (bases 54264 to 55012)
   AUTHOR (AU):         Babst,M.; Wendland,B.; Estepa,E.J.; Emr,S.D.
   TITLE (TI):          The Vps4p AAA ATPase regulates membrane association of
                        a Vps protein complex required for normal endosome
                        function
   JOURNAL (SO):        EMBO J., 17 (11), 2982-2993 (1998)
   OTHER SOURCE (OS):   CA 129:146701
REFERENCE:              54 (bases 149275 to 150765)
   AUTHOR (AU):         Silve,S.; Dupuy,P.H.; Ferrara,P.; Loison,G.
   TITLE (TI):          Human lamin B receptor exhibits sterol C14-reductase
                        activity in Saccharomyces cerevisiae
   JOURNAL (SO):        Biochim. Biophys. Acta, 1392 (2-3), 233-244 (1998)
   OTHER SOURCE (OS):   CA 129:146116
REFERENCE:              55 (bases 27949 to 28578)
   AUTHOR (AU):         Caldas,C.; Kim,M.H.; MacGregor,A.; Cain,D.;
                        Aparicio,S.; Wiedemann,L.M.
   TITLE (TI):          Isolation and characterization of a pufferfish MLL
                        (mixed lineage leukemia)-like gene (fMll) reveals
                        evolutionary conservation in vertebrate genes related
                        to Drosophila trithorax
   JOURNAL (SO):        Oncogene, 16 (25), 3233-3241 (1998)
   OTHER SOURCE (OS):   CA 129:171330
REFERENCE:              56 (bases 218542 to 219708)
   AUTHOR (AU):         Rayner,J.C.; Munro,S.
   TITLE (TI):          Identification of the MNN2 and MNN5
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                            mannosyltransferases required for forming and extending
                            the mannose branches of the outer chain mannans of
                            Saccharomyces cerevisiae
    JOURNAL (SO):           J. Biol. Chem., 273 (41), 26836-26843 (1998)
    OTHER SOURCE (OS):      CA 130:22764
REFERENCE:                  57 (bases 218542 to 219708)
    AUTHOR (AU):            Lussier,M.; Sdicu,A.M.; Bussey,H.
    TITLE (TI):             The KTR and MNN1 mannosyltransferase families of
                            Saccharomyces cerevisiae
    JOURNAL (SO):           Biochim. Biophys. Acta, 1426 (2), 323-334 (1999)
    OTHER SOURCE (OS):      CA 130:293055
REFERENCE:                  58 (bases 154037 to 156562)
    AUTHOR (AU):            de Vries,R.P.; Visser,J.; de Graaff,L.H.
    TITLE (TI):             CreA modulates the XlnR-induced expression on xylose of
                            Aspergillus niger genes involved in xylan degradation
    JOURNAL (SO):           Res. Microbiol., 150 (4), 281-285 (1999)
    OTHER SOURCE (OS):      CA 131:180701
REFERENCE:                  59 (bases 80610 to 81592)
    AUTHOR (AU):            Ui,S.; Mimura,A.; Ohkuma,M.; Kudo,T.
    TITLE (TI):             Formation of a chiral acetoinic compound from diacetyl
                            by Escherichia coli expressing meso-2,3-butanediol
                            dehydrogenase
    JOURNAL (SO):           Lett. Appl. Microbiol., 28 (6), 457-460 (1999)
    OTHER SOURCE (OS):      CA 131:225912
REFERENCE:                  60 (bases 211445 to 212528)
    AUTHOR (AU):            Krappmann,S.; Helmstaedt,K.; Gerstberger,T.; Eckert,S.;
                            Hoffmann,B.; Hoppert,M.; Schnappauf,G.; Braus,G.H.
    TITLE (TI):             The aroC gene of Aspergillus nidulans codes for a
                            monofunctional, allosterically regulated chorismate
                            mutase
    JOURNAL (SO):           J. Biol. Chem., 274 (32), 22275-22282 (1999)
    OTHER SOURCE (OS):      CA 131:268796
REFERENCE:                  61 (bases 137703 to 138530)
    AUTHOR (AU):            Lombaerts,M.; Peltola,P.H.; Visse,R.; den Dulk,H.;
                            Brouwer,J.
    TITLE (TI):             Characterization of the rhp7(+) and rhp16(+) genes in
                            Schizosaccharomyces pombe
    JOURNAL (SO):           Nucleic Acids Res., 27 (17), 3410-3416 (1999)
    OTHER SOURCE (OS):      CA 132:809
REFERENCE:                  62
    AUTHOR (AU):            Tsai,H.F.; Wheeler,M.H.; Chang,Y.C.; Kwon-Chung,K.J.
    TITLE (TI):             A developmentally regulated gene cluster involved in
                            conidial pigment biosynthesis in Aspergillus fumigatus
    JOURNAL (SO):           J. Bacteriol., 181 (20), 6469-6477 (1999)
    OTHER SOURCE (OS):      CA 132:45624
REFERENCE:                  63
    AUTHOR (AU):            DeZwaan,T.M.; Carroll,A.M.; Valent,B.; Sweigard,J.A.
    TITLE (TI):             Magnaporthe grisea pth11p is a novel plasma membrane
                            protein that mediates appressorium differentiation in
                            response to inductive substrate cues
    JOURNAL (SO):           Plant Cell, 11 (10), 2013-2030 (1999)
    OTHER SOURCE (OS):      CA 132:47358
REFERENCE:                  64 (bases 20272 to 22263)
    AUTHOR (AU):            Layfield,R.; Franklin,K.; Landon,M.; Walker,G.;
                            Wang,P.; Ramage,R.; Brown,A.; Love,S.; Urquhart,K.;
                            Muir,T.; Baker,R.; Mayer,R.J.
    TITLE (TI):             Chemically synthesized ubiquitin extension proteins
                            detect distinct catalytic capacities of
                            deubiquitinating enzymes
    JOURNAL (SO):           Anal. Biochem., 274 (1), 40-49 (1999)
    OTHER SOURCE (OS):      CA 132:20406
REFERENCE:                  65 (bases 55690 to 56601)
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   AUTHOR (AU):          Munoz,M.J.; Bejarano,E.R.; Daga,R.R.; Jimenez,J.
   TITLE (TI):           The identification of Wos2, a p23 homologue that
                         interacts with Wee1 and Cdc2 in the mitotic control of
                         fission yeasts
   JOURNAL (SO):         Genetics, 153 (4), 1561-1572 (1999)
   OTHER SOURCE (OS):    CA 132:177833
REFERENCE:               66 (bases 149275 to 150765)
   AUTHOR (AU):          Zweytick,D.; Hrastnik,C.; Kohlwein,S.D.; Daum,G.
   TITLE (TI):           Biochemical characterization and subcellular
                         localization of the sterol C-24(28) reductase, erg4p,
                         from the yeast saccharomyces cerevisiae
   JOURNAL (SO):         FEBS Lett., 470 (1), 83-87 (2000)
   OTHER SOURCE (OS):    CA 132:331762
REFERENCE:               67 (bases 51277 to 53277)
   AUTHOR (AU):          Cole,C.N.
   TITLE (TI):           mRNA export: the long and winding road
   JOURNAL (SO):         Nat. Cell Biol., 2 (4), E55-E58 (2000)
   OTHER SOURCE (OS):    CA 133:27711
REFERENCE:               68 (bases 51277 to 53277)
   AUTHOR (AU):          Stutz,F.; Bachi,A.; Doerks,T.; Braun,I.C.; Seraphin,B.;
                         Wilm,M.; Bork,P.; Izaurralde,E.
   TITLE (TI):           REF, an evolutionary conserved family of hnRNP-like
                         proteins, interacts with TAP/Mex67p and participates in
                         mRNA nuclear export
   JOURNAL (SO):         RNA, 6 (4), 638-650 (2000)
   OTHER SOURCE (OS):    CA 133:70318
REFERENCE:               69 (bases 163244 to 165037)
   AUTHOR (AU):          Loubradou,G.; Turcq,B.
   TITLE (TI):           Vegetative incompatibility in filamentous fungi: a
                         roundabout way of understanding the phenomenon
   JOURNAL (SO):         Res. Microbiol., 151 (4), 239-245 (2000)
   OTHER SOURCE (OS):    CA 133:234784
REFERENCE:               70 (bases 166037 to 167516)
   AUTHOR (AU):          Yu,J.; Woloshuk,C.P.; Bhatnagar,D.; Cleveland,T.E.
   TITLE (TI):           Cloning and characterization of avfA and omtB genes
                         involved in aflatoxin biosynthesis in three Aspergillus
                         species
   JOURNAL (SO):         Gene, 248 (1-2), 157-167 (2000)
   OTHER SOURCE (OS):    CA 133:345391
REFERENCE:               71 (bases 143978 to 145355)
   AUTHOR (AU):          Sanders,P.M.; Lee,P.Y.; Biesgen,C.; Boone,J.D.;
                         Beals,T.P.; Weiler,E.W.; Goldberg,R.B.
   TITLE (TI):           The arabidopsis DELAYED DEHISCENCE1 gene encodes an
                         enzyme in the jasmonic acid synthesis pathway
   JOURNAL (SO):         Plant Cell, 12 (7), 1041-1061 (2000)
   OTHER SOURCE (OS):    CA 134:25937
REFERENCE:               72 (bases 145510 to 146577)
   AUTHOR (AU):          Cheng,Q.; Thomas,S.M.; Kostichka,K.; Valentine,J.R.;
                         Nagarajan,V.
   TITLE (TI):           Genetic analysis of a gene cluster for cyclohexanol
                         oxidation in Acinetobacter sp. Strain SE19 by in vitro
                         transposition
   JOURNAL (SO):         J. Bacteriol., 182 (17), 4744-4751 (2000)
   OTHER SOURCE (OS):    CA 134:37832
REFERENCE:               73 (bases 163244 to 165037)
   AUTHOR (AU):          Saupe,S.J.
   TITLE (TI):           Molecular genetics of heterokaryon incompatibility in
                         filamentous ascomycetes
   JOURNAL (SO):         Microbiol. Mol. Biol. Rev., 64 (3), 489-502 (2000)
   OTHER SOURCE (OS):    CA 134:27321
REFERENCE:               74 (bases 128987 to 130729)
   AUTHOR (AU):          Tanaka,A.; Tsuge,T.
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       TITLE (TI):          Structural and functional complexity of the genomic
                            region controlling AK-toxin biosynthesis and
                            pathogenicity in the Japanese pear pathotype of
                            Alternaria alternata
       JOURNAL (SO):        Mol. Plant Microbe Interact., 13 (9), 975-986 (2000)
       OTHER SOURCE (OS):   CA 134:96037
   REFERENCE:               75 (bases 143978 to 145355)
       AUTHOR (AU):         Stintzi,A.; Browse,J.
       TITLE (TI):          The Arabidopsis male-sterile mutant, opr3, lacks the
                            12-oxophytodienoic acid reductase required for
                            jasmonate synthesis
       JOURNAL (SO):        Proc. Natl. Acad. Sci. U.S.A., 97 (19), 10625-10630
                            (2000)
       OTHER SOURCE (OS):   CA 133:293530
   REFERENCE:               76 (bases 54264 to 55012)
       AUTHOR (AU):         Amerik,A.Y.; Nowak,J.; Swaminathan,S.; Hochstrasser,M.
       TITLE (TI):          The Doa4 deubiquitinating enzyme is functionally linked
                            to the vacuolar protein-sorting and endocytic pathways
       JOURNAL (SO):        Mol. Biol. Cell, 11 (10), 3365-3380 (2000)
       OTHER SOURCE (OS):   CA 134:82296
   REFERENCE:               77 (bases 208451 to 210658)
       AUTHOR (AU):         Tieu,Q.; Nunnari,J.
       TITLE (TI):          Mdv1p is a WD repeat protein that interacts with the
                            dynamin-related GTPase, Dnm1p, to trigger mitochondrial
                            division
       JOURNAL (SO):        J. Cell Biol., 151 (2), 353-366 (2000)
       OTHER SOURCE (OS):   CA 134:52741
   REFERENCE:               78 (bases 208451 to 210658)
       AUTHOR (AU):         Mozdy,A.D.; McCaffery,J.M.; Shaw,J.M.
       TITLE (TI):          Dnm1p GTPase-mediated mitochondrial fission is a
                            multi-step process requiring the novel integral
                            membrane component Fis1p
       JOURNAL (SO):        J. Cell Biol., 151 (2), 367-380 (2000)
       OTHER SOURCE (OS):   CA 134:52934
   REFERENCE:               79 (bases 94126 to 97982)
       AUTHOR (AU):         Kadoya,T.; Kishida,S.; Fukui,A.; Hinoi,T.; Michiue,T.;
                            Kikuchi,A.
       TITLE (TI):          Inhibition of Wnt signaling pathway by a novel
                            axin-binding protein
       JOURNAL (SO):        J. Biol. Chem., 275 (47), 37030-37037 (2000)
       OTHER SOURCE (OS):   CA 134:233219
   REFERENCE:               80 (bases 80610 to 81592)
       AUTHOR (AU):         Ui,S.; Takusagawa,Y.; Ohtsuki,T.; Mimura,A.; Ohkuma,M.;
                            Kudo,T.
       TITLE (TI):          Stereochemical applications of the expression of the
                            L-2,3-butanediol dehydrogenase gene in Escherichia coli
       JOURNAL (SO):        Lett. Appl. Microbiol., 32 (2), 93-98 (2001)
       OTHER SOURCE (OS):   CA 135:353434
   REFERENCE:               81 (bases 80610 to 81592)
       AUTHOR (AU):         Otagiri,M.; Kurisu,G.; Ui,S.; Takusagawa,Y.; Ohkuma,M.;
                            Kudo,T.; Kusunoki,M.
       TITLE (TI):          Crystal structure of meso-2,3-butanediol dehydrogenase
                            in a complex with NAD+ and inhibitor mercaptoethanol at
                            1.7 A resolution for understanding of chiral substrate
                            recognition mechanisms
       JOURNAL (SO):        J. Biochem., 129 (2), 205-208 (2001)
       OTHER SOURCE (OS):   CA 135:2180
   REFERENCE:               82 (bases 41237 to 43709)
       AUTHOR (AU):         Davidson,E.; Caffarella,J.; Vitseva,O.; Hou,Y.M.;
                            King,M.P.
       TITLE (TI):          Isolation of two cDNAs encoding functional human
                            cytoplasmic cysteinyl-tRNA synthetase
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JOURNAL (SO):   Biol. Chem., 382 (3), 399-406 (2001)
   OTHER SOURCE (OS): CA 135:118589
REFERENCE: 83 (bases 119272 to 121189)
   AUTHOR (AU):   Cukovic,D.; Ehlting,J.; VanZiffle,J.A.; Douglas,C.J.
   TITLE (TI):   Structure and evolution of 4-coumarate:coenzyme A
                       ligase (4CL) gene families
   JOURNAL (SO):   Biol. Chem., 382 (4), 645-654 (2001)
   OTHER SOURCE (OS): CA 136:145906
REFERENCE: 84 (bases 87776 to 89339)
   AUTHOR (AU):   Gassama-Diagne,A.; Hullin-Matsuda,F.; Li,R.Y.;
                       Nauze,M.; Ragab,A.; Pons,V.; Delagebeaudeuf,C.;
                       Simon,M.F.; Fauvel,J.; Chap,H.
   TITLE (TI):   Enterophilins, a new family of leucine zipper proteins
                       bearing a b30.2 domain and associated with enterocyte
                       differentiation
   JOURNAL (SO):   J. Biol. Chem., 276 (21), 18352-18360 (2001)
   OTHER SOURCE (OS): CA 136:114413
REFERENCE: 85 (bases 80610 to 81592)
   AUTHOR (AU):   Otagiri,M.; Kurisu,G.; Swaminathan,S.; Ui,S.;
                       Yoneda,S.; Ohkuma,M.; Kudo,T.; Kusunoki,M.
   TITLE (TI):   Crystallization and preliminary X-ray studies of
                       meso-2,3-butanediol dehydrogenase from Klebsiella
                       pneumoniae IAM1063
   JOURNAL (SO):   Acta Crystallogr. D Biol. Crystallogr., 57 (PT 6),
                       857-859 (2001)
REFERENCE: 86 (bases 51277 to 53277)
   AUTHOR (AU):   Zenklusen,D.; Vinciguerra,P.; Strahm,Y.; Stutz,F.
   TITLE (TI):   The yeast hnRNP-Like proteins Yra1p and Yra2p
                       participate in mRNA export through interaction with
                       Mex67p
   JOURNAL (SO):   Mol. Cell. Biol., 21 (13), 4219-4232 (2001)
   OTHER SOURCE (OS): CA 135:177841
REFERENCE: 87 (bases 1 to 226503)
   AUTHOR (AU):   Pel,H.J.; de Winde,J.H.; Archer,D.B.; Dyer,P.S.;
                       Hofmann,G.; Schaap,P.J.; Turner,G.; de Vries,R.P.;
                       Albang,R.; Albermann,K.; Andersen,M.R.; Bendtsen,J.D.;
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                       Heijden,R.T.; van der Kaaij,R.M.; Klis,F.M.;
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                       Stam,H.
   TITLE (TI):   Genome sequencing and analysis of the versatile cell
                       factory Aspergillus niger CBS 513.88
   JOURNAL (SO):   Nat. Biotechnol., 25 (2), 221-231 (2007)
   OTHER SOURCE (OS): CA 146:310276
REFERENCE: 88 (bases 1 to 226503)
   AUTHOR (AU):   Pel,H.J.
   TITLE (TI):   Direct Submission
   JOURNAL (SO):   Submitted (01-MAY-2006) Pel H.J., DSM, 624-0295, P.O.
                       Box 1, 2600 MA Delft, THE NETHERLANDS

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                                      the similarity to dma1 of S. pombe
                                      is limited to the C-terminal half
                                      of the predicted ORF; the
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                                       sequence:UniProtKB:NCX4G11.7"
                                       /note="unnamed protein product;
                                       Title: similarity to hypothetical
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                                          /translation="MSGLMHKVKDAVTGHHKESS
                                          NTNTSNTSSNAGPHSSNMANKMDP
                                          RVDSDRDNRARHEAMGGAHGPHDSSMANKMDPRV
                                          DSDRDNRANPSGGLGGSGAGYSSG
                                          GYSSGPHESGMANKMDPRVDSDRDNRARHQAMGG
                                          AHGPHDSSMANKMDPRVDSDRDNR
                                          AAGGYSGTHTTGAGYGGAGAGAGYGGGAGYGGSG
                                          VNDYTTSSGYGGSSNAGPHGSNMA
                                          NKMDPRVDSDMDNRARHQGMASSSYNAPGQTTAG
                                          PHSSNMANKLDPRVDSDLDNRGTL GTQRGF"
exon              complement(6405..6781)  /locus-tag="An14g05070"
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intron            complement(6782..6839)  /locus-tag="An14g05070"
                                          /number=1
exon              complement(6840..7160)  /locus-tag="An14g05070"
                                          /number=2
intron            complement(7161..7214)  /locus-tag="An14g05070"
                                          /number=2
exon              complement(7215..7365)  /locus-tag="An14g05070"
                                          /number=3
gene              complement(<8900..>1022 /locus-tag="An14g05080"
                  6)
mRNA              complement(join(<8900.. /locus-tag="An14g05080"
                  9282,9368..9550,
                  9634..9898,
                  10206..>10226))
CDS               complement(join(8900..9 /locus-tag="An14g05080"
                  282,9368..9550,
                  9634..9898,
                  10206..10226))
                                          /inference="profile:COGS:COG0666"
                                          /inference="profile:PFAM:PF00023"
                                          /note="unnamed protein product;
                                          Function: many ankyrin repeat
                                          regions are known to function as
                                          protein-protein interaction
                                          domains. Remark: closest manual
                                          BLASTP homologue:
                                          SWISSPROT:ANK1-HUMAN. Similarity:
                                          ankyrin repeats (ANK) are tandemly
                                          repeated modules of about 33 amino
                                          acids, that occur in a large
                                          number of functionally diverse
                                          proteins mainly from eukaryotes.
                                          Similarity: the predicted ORF
                                          shows similarity also to the ZU5
                                          domain present in ZO-1 and
                                          Unc5-like netrin receptors, which
                                          function remains unknown.
                                          Similarity: the similarity to
                                          ankyrin of H. sapiens and other
                                          proteins is mainly due to the
                                          presence of two ankyrin repeats.
                                          Title: weak similarity to ankyrin
                                          (variant 2.1) -Homo sapiens"
                                          /citation=[5]
                                          /codon-start=1
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                                          PTSSNGHTPAIVETLRIELLNGLM
                                          GPASGSLITVISESGEKTMRRVFSGFQPILAVGN
                                          PSLANYLVDELRPSSEKTAHRGHE
                                          SIIRILLDFGVKDLNSRDKSGHTPLLHAASMWHT
                                          KIVKLLLRTGIPDPNCQNAGAHET
                                          IMFGHRWPLPVKLVMKRSLPLLETGKMDSSLEDQ
                                          DGFTPLTYATEYGNERIIKLLLDA
                                          SDPRAAKTATTELEIFAATRATPELQPVHEGPVV
                                          EATPSELVSRTSPKDIVRLRWRNN PALNPQH"
exon              complement(8900..9282)    /locus-tag="An14g05080"
                                          /number=1
intron            complement(9283..9367)    /locus-tag="An14g05080"
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exon              complement(9368..9550)    /locus-tag="An14g05080"
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intron            complement(9551..9633)    /locus-tag="An14g05080"
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exon              complement(9634..9898)    /locus-tag="An14g05080"
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intron            complement(9899..10205)   /locus-tag="An14g05080"
                                          /number=3
exon              complement(10206..10226   /locus-tag="An14g05080"
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gene              <11182..>11344           /locus-tag="An14g05090"
mRNA              join(<11182..11234,       /locus-tag="An14g05090"
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CDS               join(11182..11234,        /locus-tag="An14g05090"
                  11281..11344)

                                          /note="Similarity: BLASTP
                                          identifies a stretch of similarity
                                          to D. melanogaster genomic
                                          fragment CG6456; there is no
                                          sufficient reason to consider such
                                          a similarity significant."
                                          /codon-start=1
                                          /product="hypothetical protein"
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exon              11182..11234             /locus-tag="An14g05090"
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intron            11235..11280             /locus-tag="An14g05090"
                                          /number=1
exon              11281..11344             /locus-tag="An14g05090"
                                          /number=2
gene              <12054..>13438           /locus-tag="An14g05100"
mRNA              join(<12054..12184,       /locus-tag="An14g05100"
                  12254..12395,
                  12454..12995,
                  13054..>13438)
CDS               join(12054..12184,        /locus-tag="An14g05100"
                  12254..12395,
                  12454..12995,
                  13054..13438)

                                          /inference="profile:COGS:COG3781"
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sequence:PIR:AD2179"
/note="unnamed protein product;
Title: strong similarity to
hypothetical protein alr2987 –
Nostoc sp"
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LNNAHHYRAGTHPHLLTSRSKPRR
WPLVFRFIKGAIHAAILLPVFLHAAFTAFVVYLD
VYVFDTVGLPSSIIPSLSIVVGLM
LVFRNQTSYNRFWDGRNGMNTIYTCIRNLVRTIV
TNGYSTAGPPTAAEKEDIERTIRI
LMSIPFAVKNHLRAEWGAAWALGNDVAENGVAAF
NPDYASLLPAGLVGHEDEGLGLPF
QLTFFVDGFIKRGVERGWFNAPGASQMQAQLNSL
MDAYGKMETIKLTPIPVAHLIHQK
QVLALFGCVLPFGMVDDMGWWTVPMVSLVIFTLY
GIEGIGSQLEDPFGYDRNDIKMDA
IVGDAKTEIDVVLAEWRRLMASLESATDNGDQHL
GNGLVVEEEVKEPKFMPPDMFLKH RARPSGR"

exon	12054..12184	/locus-tag="An14g05100" /number=1	
intron	12185..12253	/locus-tag="An14g05100" /number=1	
exon	12254..12395	/locus-tag="An14g05100" /number=2	
intron	12396..12453	/locus-tag="An14g05100" /number=2	
exon	12454..12995	/locus-tag="An14g05100" /number=3	
intron	12996..13053	/locus-tag="An14g05100" /number=3	
exon	13054..13438	/locus-tag="An14g05100" /number=4	
gene	<13882..>14418	/locus-tag="An14g05110"	
mRNA	<13882..>14418	/locus-tag="An14g05110"	
CDS	13882..14418	/locus-tag="An14g05110"	

/inference="similar to AA
sequence:UniProtKB:BT004329.1"
/note="unnamed protein product;
Similarity: the predicted ORF
contains an EF-hand,the most
common domain responsible for
calcium binding in proteins like
calmodulin, myosin regulatory
light chains,parvalbumins,
troponins C, and neuronal calcium
sensors. Title: weak similarity to
hypothetical protein AT4g01140 –
Arabidopsis thaliana"
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/protein-id="CAK42072.1"
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LEKFSSIHASQSQSSTTTTTLANGTTITVTNTT
SSAAIEKIEGVKALLLSSQEKIYG
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VLDQLVDTLECVLSFATGLLETIL
DGLFDLLKTIIEGVEKLL"

sig-peptide	13882..13941	/locus-tag="An14g05110"
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mat-peptide	13942..14415	/locus-tag="An14g05110"
		/product="unnamed"
exon	13882..14418	/locus-tag="An14g05110"
		/number=1
gene	complement(<14885..>163	/locus-tag="An14g05120"
	07)	
mRNA	complement(join(<14885.	/locus-tag="An14g05120"
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	15370..15531,	
	15585..15698,	
	15751..15900,	
	15955..16104,	
	16161..>16307))	
CDS	complement(join(14885..	/locus-tag="An14g05120"
	15101,15159..15313,	
	15370..15531,	
	15585..15698,	
	15751..15900,	
	15955..16104,	
	16161..16307))	
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		/inference="similar to AA
		sequence:UniProtKB:NC17E5.27"
		/note="unnamed protein product;
		Function: MoxR is a poorly
		characterized bacterial protein
		which may be involved in the
		regulation of formation of active
		methanol dehydrogenase.
		Similarity: the predicted ORF
		shows weak similarity to many
		putative proteins classified as
		MoxR-like ATPases. Title: strong
		similarity to hypothetical
		conserved protein 17E5.290 –
		Neurospora crassa"
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		/protein-id="CAK42073.1"
		/db-xref="GI:134081818"
		/translation="MEDGSEISRLAPELSDLEVA
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		KELALICTNTFGLSYSILDCSSATSLDDFRAELL
		PPGVYRSSYARPSRSRLTTESAGM
		ISSYHDLRDHKGRLKSAPIEHKQEVVNVVIAKNF
		NHVNDNIQREALELMHSKQLTTPA
		GVLEAPNNFLFLPLIVRDETHPINPHLNDYLFIS
		HFHDTEDGYVYLEENNDWLSDGQL
		SASSVIHKPEAQMKKGHPYVDSTLLGQLQQLSTT
		VSMGADIARYQQDIVVFLRLSRAV
		AGGISTRSNLYFKSFSKLLAVLHGIDFLTPSIVA
		LAARKVFRHRIIVAKPEEDRSLQY
		GSDLHAVSQVLEYANPDSILDGVLTLEAPL"
exon	complement(14885..15101	/locus-tag="An14g05120"
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intron	complement(15102..15158	/locus-tag="An14g05120"
	)	
		/number=1
exon	complement(15159..15313	/locus-tag="An14g05120"

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                                                    /number=2
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                                                    /number=3
         intron              complement(15532..15584 /locus-tag="An14g05120"
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                                                    /number=3
         exon                complement(15585..15698 /locus-tag="An14g05120"
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                                                    /number=4
         intron              complement(15699..15750 /locus-tag="An14g05120"
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                                                    /number=4
         exon                complement(15751..15900 /locus-tag="An14g05120"
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                                                    /number=5
         intron              complement(15901..15954 /locus-tag="An14g05120"
                              )
                                                    /number=5
         exon                complement(15955..16104 /locus-tag="An14g05120"
                              )
                                                    /number=6
         intron              complement(16105..16160 /locus-tag="An14g05120"
                              )
                                                    /number=6
         exon                complement(16161..16307 /locus-tag="An14g05120"
                              )
                                                    /number=7
         gene                <16557..>19301          /locus-tag="An14g05130"
         mRNA                join(<16557..16701,     /locus-tag="An14g05130"
                              16758..16864,
                              16910..17038,
                              17088..17676,
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                              19053..>19301)
         CDS                 join(16557..16701,      /locus-tag="An14g05130"
                              16758..16864,
                              16910..17038,
                              17088..17676,
                              17726..18996,
                              19053..19301)
                                                    /inference="profile:PFAM:PF04840"
                                                    /inference="profile:PFAM:PF04841"
                                                    /note="unnamed protein product;
                                                    Complex: VPS16 of S. cerevisiae is
                                                    a component of the so called class
                                                    C Vps complex, required for
                                                    vacuolar protein sorting and
                                                    morphology. Function: VPS16 of S.
                                                    cerevisiae is required for
                                                    vacuolar protein sorting and
                                                    vacuolar biogenesis and stability.
                                                    Phenotype: S. cerevisiae VPS16
                                                    mutants have pleiotropic defects
                                                    in vacuolar morphology and
                                                    vacuolar protein targeting. Title:
                                                    strong similarity to vacuolar
                                                    protein sorting-associated protein
```

Vps16 - Saccharomyces cerevisiae
vacuole"
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/citation=[11]
/citation=[13]
/citation=[42]
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GGAIALHRDESKPYRFRDAQTAKSSIDIYSCSGK
HINRINWEYGTIRGLGWSDKEELL
VITEDGTVRRYFGLHGDFTSFSLGNGAEDYGVRA
CRFWTSGFVALLSNNQLVAVSNYD
EPRPRLLAPCPEGEVSSWSLIPPAYTLSRSVEVL
LAVDKTVYLVDPTEAEDKVLQNGP
FKHASVSPTGRFVALITAEGKVWVVSSDFQSKYS
EYDPESRVTPRTVDWCGDDAVVIA
WEDEVHLIGPNGVAARYYYDGTVHVVPEFDGVRL
ITNDTCEFLHKVVDVTEAIFRLGS
TSPASVLLDSIDLLEKKSPKADENIQRIRPSLPE
AVDTCVKAAGHEFDTYWQKRLLKA
ASFGKSVLDLYNSDEFVEMTEKLRVLKAVRDYQI
GLPLSYEQYMRLTPERLIERLVNR
HEYLLAIRISEYLELPADRIYVHWASQKVKVSTV
DDDAVCKLIVQRLEGKPGISFELI
AQTAYDEGRAHLATQLLNHEPRAGKQVPLLLDME
EDEIALDKAIESGDVDLVNYVLLH
LKTKLPLASFFRTINTRPMASALVETTARGQDTE
LLKDLFYQDDRPIDGSNVLLSEAL
DATDLPRKTEKLQLASRLLSDSKDPSVVLQQKLL
NEASQLLKVQEALDKDLADRSEFL
GLSLNETIYRLIRSGYGKRAQKIQSEFRMPEKTF
WWLRLRALVAKRDWGELEEIGKNK
KSPIGWEPFYNEILGAGNTKLASLFVPKCTNLPA
EDKMEMWVKCGMIAKAGEEAFRAK
NVNALELLQARASGPAAVEIERMINQLRPRK"

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exon	16758..16864	/locus-tag="An14g05130"
		/number=2
intron	16865..16909	/locus-tag="An14g05130"
		/number=2
exon	16910..17038	/locus-tag="An14g05130"
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intron	17039..17087	/locus-tag="An14g05130"
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exon	17726..18996	/locus-tag="An14g05130"
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		/number=5
exon	19053..19301	/locus-tag="An14g05130"
		/number=6
gene	complement(<19354..>199	/locus-tag="An14g05140"
	96)	

mRNA	complement(join(<19354. .19554,19615..19907, 19981..>19996))	/locus-tag="An14g05140"
CDS	complement(join(19354.. 19554,19615..19907, 19981..19996))	/locus-tag="An14g05140"
		/note="unnamed protein product; Phenotype: ECM1 mutation in S. cerevisiae causes perturbation of the cell surface. Remark: ECM1 of S. cerevisiae is also called YAL059w. Title: similarity to Ecm1 - Saccharomyces cerevisiae" /citation=[39] /codon-start=1 /protein-id="CAK42075.1" /db-xref="GI:134081820" /translation="MAKSRPQSKHSRAARRAASP SLDVDKSLTSLPRAEETTVQRDSI LSERANAGVSKKQSKGKAKTRAQRLRQQKGVERA EAVMDQLEKKVTKSEVRAKSVKAR RAEWEDLNRKTKSMFEALNEEADDNMDDAMVDDA AASKPAKRSKPAPVTQTPVVEEHE GIDVDDDIT"
exon	complement(19354..19554)	/locus-tag="An14g05140"
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intron	complement(19555..19614)	/locus-tag="An14g05140"
		/number=1
exon	complement(19615..19907)	/locus-tag="An14g05140"
		/number=2
intron	complement(19908..19980)	/locus-tag="An14g05140"
		/number=2
exon	complement(19981..19996)	/locus-tag="An14g05140"
		/number=3
gene	<20272..>22263	/locus-tag="An14g05150"
mRNA	<20272..>22263	/locus-tag="An14g05150"
CDS	20272..22263	/locus-tag="An14g05150" /EC-number="3.1.2.15" /inference="profile:COGS:COG5533" /inference="profile:COGS:COG5560" /inference="profile:PFAM:PF00443" /inference="similar to AA sequence:PIR:S67665" /note="unnamed protein product; Catalytic activity: ubiquitin C-terminal thiolester + H2O = ubiquitin + thiol. Function: UBP1 of S. cerevisiae has an ATP-independent isopeptidase activity, cleaving at the carboxyl terminus of the ubiquitin moiety in natural or engineered linear fusion proteins, irrespective of their size or the presence of an amino-terminal extension to ubiquitin. Similarity: UBP1 belongs to peptidase family C19;

also known as family 2 of
ubiquitin carboxyl-terminal
hydrolases. Similarity: although
the predicted ORF is shorter than
UBP1 of S. cerevisiae and the
alignment contains several gaps,
it shows consistent similarity to
several ubiquitin-specific
processing proteases. Title:
similarity to ubiquitin specific
protease Ubp1 - Saccharomyces
cerevisiae"
/citation=[7]
/citation=[12]
/citation=[27]
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ITLYLAVSYLGPASLSVARIAWNILVYLTPSRLI
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AMQRILGLDDTSFSSLFPRAPAFSSFGTSLLSSK
NNVPPGLGNWDNSCYQNSIIQGLA
SLQSLERFLDQNVEQLGQKALLSTHQALKDIIER
LNSADSNGQRLWTPADLKSMSSWQ
QQDAQEYFSKIVDQLDLEVQQATRRHTRNLGLKM
AGPQEHVIGSGISQELQESSAGET
RITGNQIFRNPLEGLLAQRVGCIQCGWTEGLSLI
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MHLEPIEGVECAKCTLLRVQSQLLNLLKQIGDDE
ETPSATPESPKISDALRSSAQERL
QAVEQALEEEDFAEKTLSQKCHIPGKNRVSSTKS
RQAVVARPPQCLVIHVNRSMFDEN
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GHYQLRAVITHYGRHENGHYICYRKYPTDTFPAH
VPDAIIEADGDKERDERWYRLSDE
DVQMVSEANVMSQGGAFMLFYEAVEDYSPEAAED
VDSGLAEEEGSAPSSSCTPSETMS
TTSAATGDSTSDVSQATSVSTALNVEPRVEKSLL
MSDVD"

centrosome separation at the time
of mitosis. Localization: human
centrin is localized at the
centrosome of interphase cells and
redistributes to the region of the
spindle poles during mitosis.
Similarity: in the predicted ORF
the EF-hands are not well
conserved; this fact might have
important functional consequences.
Similarity: the human centrin
sequence has four putative
calcium-binding domains as defined
by the EF-hand consensus. Title:
similarity to centrin - Homo
sapiens centrosome"
/citation=[16]
/codon-start=1
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/db-xref="GI:134081822"
/translation="MPPKKRSAPSSGPAPKRARQ
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SETVEEFADQKEGVIPRGDVRKALVALGLDPTDS
EELHSIIEAVDPTDTGYVPYEPFL
AVAAAKLRSRSDDAMAAEVDAAYRLFTRGSGGVI
TLNHLRRIARELKEEELGDELLKD
MILEANGGAGVHAGVTLEQFHDVMTRAGVF"

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exon	complement(23085..23287)	/locus-tag="An14g05160"
		/number=2
intron	complement(23288..23362)	/locus-tag="An14g05160"
		/number=2
exon	complement(23363..23365)	/locus-tag="An14g05160"
		/number=3
gene	<23835..>25756	/locus-tag="An14g05170"
mRNA	join(<23835..23848, 23890..23947, 24000..24221, 24272..>25756)	/locus-tag="An14g05170"
CDS	join(23835..23848, 23890..23947, 24000..24221, 24272..25756)	/locus-tag="An14g05170"

/EC-number="1.-.-.-"
/inference="profile:COGS:COG3118"
/inference="profile:PFAM:PF00085"
/note="unnamed protein product;
Function: thioredoxin participates
in various redox reactions through
the reversible oxidation of its
active center dithiol to a
disulfide, and catalyzes
dithiol-disulfide exchange
reactions. Similarity: the main

feature of the predicted ORF,as
well as of the very similar N.
crassa hypothetical protein 17E5.
270, is to contain different
structural domains, including the
thioredoxin and the leucine
zippers in the C-terminal region.
Similarity: the similarity to
chicken thioredoxin and similar
proteins of other species is
limited to a single domain of the
predicted ORF. Title: similarity
to thioredoxin - Gallus gallus"
/citation=[1]
/codon-start=1
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/db-xref="GI:134081823"
/db-xref="GOA:A2R3R0"
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LARMYSLALTGTQIDAIYHTSLVL
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LPLDVIEEYIQSLAEIYTPESYDL
FLHNCNNFTQDLAMFALGKGIPEHIQNLPQTFLS
TPFGQMMKPQIEMALRGVTQGTGA
GTGTVGTQTPTTSAPTAPAQPAPVTQGSVRIASN
LAQLEHHLAAAADSCAVIFFTSAT
CPPCKMVYPTYDELAEEAGAKATLIKVDISTAMD
VSMKYSVRATPTFMTFLKGQKLDE
WSGANPAQLRGNVRLLLEMAHPPHRHQQLRLPSL
QRPITNYVTYKKVPPLDKLVQKLD
PHHEDPRLLSMITYLKHRTSSSTPAADTPLPQDL
PSFATYLQTTCGFLALDHLFALVD
LTRLLFLDPRVSGYFAEEPGHTTLLTLLSPSAGL
SGCPYNLRIVMLQLCCTLFSTPLY
RDQLTTSSSLLPTLLHLTTSSLLDSHTNLRVVAA
SLAYNLAALNHNARFAGHADPLSE
ESQVELTASLVEAITQEEESQEALHGLLFALGLL
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mRNA                   complement(join(<35692.   /locus-tag="An14g05240"
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                                               Spinosyns are insecticidal
                                               microlides which are useful for
                                               the control of arachnids,
                                               nematodes and insects. Similarity:
                                               SDR is a very large family of
                                               enzymes,most of which are known to
                                               be NAD- or NADP-dependent
                                               oxidoreductases with different
                                               specificities. Similarity: the
                                               predicted ORF shows strong
                                               similarity to several hypothetical
                                               and described members of the short
                                               chain dehydrogenase (SDR) protein
                                               family. Title: strong similarity
                                               to protein involved in spinosyn
                                               biosynthesis ORFL15 from patent
                                               WO9946387-A1 -Saccharopolyspora
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                                                Catalytic activity: ATP +
                                                L-cysteine + tRNA(cys) = AMP +
                                                pyrophosphate +
                                                L-cysteinyl-tRNA(cys). Similarity:
                                                YNL247W of S. cerevisiae belongs
                                                to class-I aminoacyl-tRNA
                                                synthetase family. Title: strong
                                                similarity to cysteine--tRNA
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                                        sequence:UniProtKB:SPBC29B5.2"
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                                        Function: isp4 of S. pombe is a
                                        membrane oligopeptide transporter.
                                        Remark: isp4 of S. pombe was
                                        originally identified by
                                        subtractive screening as gene
                                        induced during the sexual
                                        differentiation process.
                                        Similarity: the predicted A. niger
                                        protein shows strong similarity to
                                        protein isp4 of S. pombe, which
                                        belongs to the OPT subfamily of
                                        transporters specific for small
                                        oligopeptides (from the C.
                                        albicans OPT1 gene). Title: strong
                                        similarity to protein isp4p
                                        -Schizosaccharomyces pombe plasma
                                        membrane"
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gene            complement(<51277..>532 /locus-tag="An14g05300"
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mRNA            complement(join(<51277. /locus-tag="An14g05300"
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                52973..53002,
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CDS             complement(join(51277.. /locus-tag="An14g05300"
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                                    /inference="profile:PFAM:PF00076"
                                    /inference="similar to AA
                                    sequence:SWISSPROT:YRA1.YEAST"
                                    /note="unnamed protein product;
                                    Complex: YRA1 of S. cerevisiae
                                    mediates nuclear export of mRNA by
                                    interacting with several other
                                    protein factors, like Mex67.
                                    Function: YRA1 of S. cerevisiae is
                                    an mRNA-binding protein involved
                                    in the nuclear export of mRNA
                                    towards the cytoplasm. Remark:
                                    although the gene structure looks
                                    strange,the strong similarity to
                                    known proteins justify the model.
                                    Similarity: YRA1 S. cerevisiae
                                    belongs to the evolutionarily
                                    conserved REF (RNA and export
```

```
                                 factor binding proteins) family of
                                 hnRNP-like proteins. Title: strong
                                 similarity to RNA annealing
                                 protein Yra1 - Saccharomyces
                                 cerevisiae nucleus"
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                                 NGTSRGIASIVFSKPDTAAKAAKDLNGLLVDGRP
                                 MKIEVVVDASHAPEVSAPKPLGER
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gene              complement(<54264..>550  /locus-tag="An14g05310"
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mRNA              complement(join(<54264.  /locus-tag="An14g05310"
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CDS               complement(join(54264..  /locus-tag="An14g05310"
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                                    /note="unnamed protein product;
                                    Function: the S. cerevisiae
                                    homolog Did3p is a class E Vps
                                    factor, which function in the
                                    maturation of a late
                                    endosome/prevacuolar compartment
                                    into multivesicular bodies that
                                    then fuse with the vacuole.
                                    Remark: DID3 of S. cerevisiae is
                                    also called YKL041w. Remark: S.
                                    cerevisiae Did3p is probably
                                    involved in the ubiquitin-mediated
                                    maturation of multivesicular
                                    bodies. Title: strong similarity
                                    to protein involved in vacuolar
                                    protein sorting Did3 -
                                    Saccharomyces cerevisiae endosome"
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                                    EAFSVRKIQGSLKKSTGIMKDVNTLVQMPELNAT
                                    MRQLSTELVRAGIIEEMVDDAIPN
                                    NELLEEEEEAEEEVDKVLQEILHGKLSQVEGVQ
                                    PEKPLEEAPEPEDEFADQEATLEQ
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exon            complement(54965..55012  /locus-tag="An14g05310"
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mRNA            join(<55690..55720,      /locus-tag="An14g05320"
                55913..56238,
                56300..56464,
                56527..>56601)
CDS             join(55690..55720,       /locus-tag="An14g05320"
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                56300..56464,
                56527..56601)
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                                         sequence:PIR:T39220"
                                         /note="unnamed protein product;
                                         Function: WOS2 of S. pombe is a
                                         cochaperone protein that interacts
                                         with cdc2 in the control of the
                                         M-G1 transition. Similarity: WOS2
                                         of S. pombe belongs to the p23 /
                                         wos2 family. Title: strong
                                         similarity to cell cycle regulator
                                         p21 protein wos2p -
                                         Schizosaccharomyces pombe"
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                                        LLKTTQKIHFLKTDFDKWVDEDEQDEVNEDDYAN
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mRNA           join(<57642..57701,      /locus-tag="An14g05330"
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CDS            join(57642..57701,       /locus-tag="An14g05330"
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                                        Saccharomyces cerevisiae"
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                                        QGNCEKGRKCKFSHDASVERKAAKKDLYTDSRDK
                                        KDTIDDWDEEKLRKVILSKHGNPR
                                        TTTDKVCKYFIEAVENQKYGWFWTCPNGGDKCMY
                                        KHSLPPGFVLKTKEQKAAEKALMD
                                        KSPLNTLTLEDWLESERHKLTGNLTPVTPETFAK
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                                        TLFEEGNWRADDESSDEEEDDGAWNLEALRRETE
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gene	<59882..>61522	/locus-tag="An14g05340"
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CDS	join(59882..60273, 60344..60429, 60510..61189, 61367..61434, 61480..61522)	/locus-tag="An14g05340"
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sig-peptide	59882..59956	/locus-tag="An14g05340" /inference="protein motif:SignalP:2.0"
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mRNA	complement(join(<62253.	/locus-tag="An14g05350"
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	63704..>63796))	
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	62545..62677,	
	62734..63473,	
	63541..63615,	
	63704..63796))	

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                              sequence:UniProtKB:AF116902.1"
                              /note="unnamed protein product;
                              Function: ayg1 of A. fumigatus has
                              an unknown function, but it is
                              contained in the gene cluster
                              responsible for conidial
                              pigmentation. Phenotype: ayg1 null
                              mutants of A. fumigatus have
                              yellowish-green conidia. Title:
                              strong similarity to hypothetical
                              yellowish-green 1 ayg1 -
                              Aspergillus fumigatus"
                              /citation=[62]
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                              KALWETKWKFACEKSVYPFHDGAI
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                              VVYRISRFPYVDPTREDIKKEAFNRQKKVYLKAA
                              SFWKPTIQEVIIPHKHKSATDGAY
                              VPLFVRVPEHATAENPVPVVVLMTGLDGYRPDNS
                              QRTHEIINRGWATVICEIPGTADS
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gene              <63948..>65270           /locus-tag="An14g05360"
mRNA              join(<63948..64102,      /locus-tag="An14g05360"
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CDS               join(63948..64102,       /locus-tag="An14g05360"
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mRNA            join(<65395..65730, /locus-tag="An14g05370"
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                66909..>67116)
CDS             join(65395..65730,  /locus-tag="An14g05370"
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                                    Similarity: the predicted ORF
                                    shows very strong similarity to
                                    abr1 of A. fumigatus, a gene of
                                    the conidial pigmentation gene
                                    cluster; abr1 mutants have brown
                                    conidia,and the proposed function
                                    of abr1 is multicopper oxidase.
                                    Title: strong similarity to cell
                                    surface ferroxidase precursor Fet3
                                    - Saccharomyces cerevisiae plasma
                                    membrane"
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	66909..67113)	
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intron	66892..66908	/locus-tag="An14g05370"
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gene	complement(<67552..>687	/locus-tag="An14g05380"
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		Catalytic activity: the D-amino
		acid oxidase catalyzes the
		reaction: D-Amino acid + H2O + O2
		= 2-Oxo acid + NH3 + H2O2.
		Catalytic activity: the D-amino
		acid oxidase has a wide
		specificity for D-amino acids,
		acting also on glycine. Cofactor:
		D-amino acid oxidase is a
		flavoprotein (FAD is the
		cofactor). Title: strong
		similarity to D-amino acid oxidase
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		TYAHFKTLAAQEPGAGVQSTTGIEYLENPPAEYL
		NEKNIQAAYGHLDGFEYLQPGQMP
		GDVKWAVKYKTFVVNSPVYCAWLLREFVLRGGEV
		KEYTFVDLREGFYLAERVRAVVNC
		SGLGFGDEKSYIIRGQTCLVRNPCSATITRQNSD
		GSWSFCIPRPLGGGTIIGGTKQPH
		NWDPNPSMETRAQLLANAAKWFPFEEGSKEEFDV
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                                          AELEKLGDKYRLALRVAKDPRWSRVKCSHKGTYA
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exon               complement(69560..69700   /locus-tag="An14g05390"
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mRNA               <72683..>73072            /locus-tag="An14g05400"
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sig-peptide      72683..72742                    /locus-tag="An14g05400"
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                 74453..75231,
                 75292..>78401)
CDS              join(73435..73846,              /locus-tag="An14g05410"
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                                                 EMBLEST:BE760323 corresponds to
                                                 the 3' portion of the last exon
                                                 and a fragment of the putative
                                                 3'-UTR of the gene. Title: strong
                                                 similarity to hypothetical protein
                                                 CAD21189.1 - Neurospora crassa"
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                                                 IVQFLEGETWAWDVRTKHVTYEPIPTIDNPRGFA
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                                                 ESGAMFGSRRTPFDTNGIEAVRQQ
                                                 RADVASPVNRSHANSVTNSVSSKASSGMHKIPFS
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                                          EHTAVLQDKLVEQRRKELAAAELE
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                                          APTPPVPSDAGILLSDAKYQGDAE
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                                          RSRSTSRTRSMAPRRDSGGHSYGG
                                          SPVTVSIEETIENAMANQQTENPPI
                                          LPELQHLSPPPPPPPPTAPLASPRESSGTIDIA
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intron          74030..74086              /locus-tag="An14g05410"
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mRNA            complement(<78998..>803   /locus-tag="An14g05420"
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CDS             complement(78998..80320   /locus-tag="An14g05420"
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                                         ATMNVIRTLDQHQRIANRPLTQAEADATIEHSTA
                                         RLYHSRIGQPVGVLAGAIVTYKAA
                                         QNTEAWKKNFSSEAGLRRVDLLLEGIQKWARANP
                                         DTWRKEAIRAGLKTALFAFVGLML
                                         GDGIAGANDINHMMSDSRLKGLWAEARKRRDELR
                                         GHVTTGKMPPPVPTTPAPRPTGQE
                                         VPKSEEQNLPQQLGDGYGMQSGSDEEAARFGSST
                                         TSWGSETKKVATPADEAPSPSKDG
                                         NGDFWDDASPVAAEYRGKDQSMSGESAWERIRRQ
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                                         PAPAYDKPSERELAQAEFDRMLEAERKMSTDSLN
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exon            complement(78998..80320 /locus-tag="An14g05420"
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gene            complement(<80610..>815 /locus-tag="An14g05430"
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mRNA            complement(join(<80610. /locus-tag="An14g05430"
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                81545..>81592))
CDS             complement(join(80610.. /locus-tag="An14g05430"
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                81545..81592))
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                                         /inference="profile:PFAM:PF00106"
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                                         Similarity: SDR is a very large
                                         family of enzymes,most of which
                                         are known to be NAD- or
                                         NADP-dependent oxidoreductases
                                         with different specificities.
                                         Similarity: the predicted ORF
                                         shows strong similarity to several
                                         hypothetical and described members
                                         of the short chain dehydrogenase
                                         (SDR) protein family. Title:
                                         similarity to meso-2,3-butanediol
                                         dehydrogenase (D-acetoin forming)
                                         budC - Klebsiella pneumoniae"
                                         /citation=[59]
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     exon            complement(81545..81592    /locus-tag="An14g05430"
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     gene            <82379..>83449             /locus-tag="An14g05440"
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     CDS             82379..83449               /locus-tag="An14g05440"
                                     /note="unnamed protein product;
                                     Title: strong similarity to
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                                     IASASGYYKAVVKHAIGALFVILRTGMASWYKLS
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                                     RRFELVLEQSAISLFSSDRVPTFPKKYSRDTELQ
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                                     SGCQISLEKALQSSGAEYDVWDDRDKIYSHDQFM
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QVDCLKLRRTRQLTATTFEATYCG
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IGFILERLKGREAGIKDLPLCQSVLKRLHDIGIL
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mRNA	join(<85682..85731, 85821..86058, 86116..86309, 86392..>87100)	/locus-tag="An14g05460"
CDS	join(85682..85731, 85821..86058, 86116..86309, 86392..87100)	/locus-tag="An14g05460"

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/inference="similar to AA
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Title: similarity to hypothetical
protein YHR040w –Saccharomyces
cerevisiae"
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KKGGAGAGGKRKRGDGGAGGGTRAEMEFLRRAEE
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RNQCLVWTVEWILSDGEKRMRNCSETAPVADSYD
RVVPVPKEEGSDEQGQKQTGDEKP
EGTSELKTEEQQPQDAPSTTAPEPASTTEPTQPT
DAPTAQPEASNATPITSDSLPLTP
HRDLYFYLHRPRTATKQPVLAPLPPKISLAAALR
DHIVLEFPTIYVLPDSPDTIRAQE
DAKYILEEEYLRTHQSPEESSDDTGDADDAQLPP
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exon	86116..86309	/locus-tag="An14g05460"

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intron          86310..86391           /locus-tag="An14g05460"
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exon            86392..87100           /locus-tag="An14g05460"
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gene            complement(<87776..>893 /locus-tag="An14g05470"
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                                       Function: enterophilins are a new
                                       family of proteins with unknown
                                       function associated with
                                       enterocyte differentiation in C.
                                       porcellus. Title: weak similarity
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                                       Cavia porcellus"
                                       /citation=[84]
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                                       KLHATISQLRTDLITLQHETSRHLTSVFNRFSLI
                                       EARMKHSERVRFNSLAHTTHAPIT
                                       PVPVVEEDGSLQWPEYFPRTVWRFWCLKKRSRIN
                                       RLAQLAEFYQLGGYEYWGRMHQEQ
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                                       ITRPPKRQQEEAISATSSKEKPVKMARRPTVSPT
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CDS             91050..91256            /locus-tag="An14g05480"
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sig-peptide     91050..91127            /locus-tag="An14g05480"
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                                                   sequence:PIR:S19012"
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                                                   polymyxa"
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                                                   HRLDWVADMSAWYADGQLQSKSNYSVPDRPSIVA
                                                   MNLWSNGGNWSGDMKVGESVFMGI
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sig-peptide      92137..92205                      /locus-tag="An14g05490"
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mat-peptide      92206..93390                      /locus-tag="An14g05490"
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exon             92137..93393                      /locus-tag="An14g05490"
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gene             complement(<94126..>979  /locus-tag="An14g05500"
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mRNA             complement(join(<94126.  /locus-tag="An14g05500"
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CDS              complement(join(94126..  /locus-tag="An14g05500"
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                                                   /inference="similar to AA
                                                   sequence:UniProtKB:AF260129.1"
                                                   /note="unnamed protein product;
                                                   Similarity: the BLASTP alignment
                                                   is very nice, but limited to the
                                                   C-terminal part of the predicted
                                                   ORF. Title: similarity to
                                                   axin-associating molecule Axam -
                                                   Rattus norvegicus"
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                         SLWQSPMAALSEYICFGSSFPFAHPGAALVFFFT
                         LLFLLFFFFFFFFPFSPITHLPIT
                         FRRVYELSEYSNFPFLAIELVPLLSPLLSPKELV
                         SRLLLTMSGVFSTMRPSVEDHPMP
                         DVCYMPSDSAPHEEAVDNTAHDPMDCAPDSPASN
                         IPQETAKAPSAEIPKYQLRSVHVP
                         GNPKAVRLNGKHEVKPSFPLRTPLIRPDHRFSPN
                         SRAASFLGVDALQKSGRNAHSSHL
                         LSHLGTSKYLSAGLNHVSWSNNKPLSLPFGPDRS
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                         KHSGFTTPSRKRSMEGDGYEQAQPITSPSAKFRR
                         VRAGSFARSAATELEATANEDDWY
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                         SPKSRRLDASKVKPVTALAVSTTP
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                         TAVDQLGATEKVLSSSITVAPKTILKIRGRPSIS
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                         VDPWSQPTFEFPLGRAVSAVSLFYPEPKPIPEGR
                         TESVYADRWRQIQEEERQKALPSH
                         GRVSGGKTVATTLSGDPLTKRSLATCYTRGEWLN
                         DEVINGYLALIVDYLRRKNHNAGR
                         NDKPRFHAFNSFFFSNLRDKGYESVARWAKRAKI
                         GGSLLLDVDTVYIPVHNSQHWTLV
                         VVRPGERSIEHFDSLGARSRRHIAVVQTWLRGEL
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                                    involved in regulating ceramide
                                    and phosphorylated sphingoid base
                                    levels, and modulates stress
                                    responses through sphingolipid
                                    metabolites. Remark: YSR3 of S.
                                    cerevisiae is also called YKR053c.
                                    Similarity: A. niger EST
                                    EMBLEST:BE760128 comprises part of
                                    the putative 5'-UTR of the gene
                                    and part of exon 1. Title: strong
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                                    TLVILLILGLVRIHPEPADDCPCF
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mRNA	join(<103137..103259, 103323..103526, 103586..>103945)	/locus-tag="An14g05530"
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functions is the regulation of beta-1,3-glucan synthase, which synthesizes the main component of the fungal cell wall. Similarity: belongs to the ras transforming proteins. Title: strong similarity to GTP-binding protein rho1 from patent WO9738129-A1 - Candida sp"
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mRNA	complement(join(<104005..104166, 104250..104274, 104718..104893, 105194..>105283))	/locus-tag="An14g05540"	
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intron	complement(104894..1051 93)	/locus-tag="An14g05540"
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exon	complement(105194..1052 83)	/locus-tag="An14g05540"
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mRNA	join(<106070..106170, 106227..106273, 106356..106857, 106906..>107287)	/locus-tag="An14g05550"
CDS	join(106070..106170, 106227..106273, 106356..106857, 106906..107287)	/locus-tag="An14g05550"
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intron	106171..106226	/locus-tag="An14g05550"
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CDS	complement(join(107589..107677,107764..107819, 107918..107986, 108097..108183, 108460..108535, 108574..108580))	/locus-tag="An14g05560"
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sig-peptide	complement(join(108468..108535, 108574..108580))	/locus-tag="An14g05560"
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mat-peptide	complement(join(107592..107677,107764..107819, 107918..107986, 108097..108183, 108460..108467))	/locus-tag="An14g05560"
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gene	complement(<109706..>11 1182)	/locus-tag="An14g05570"
mRNA	complement(join(<109706 ..110389, 110813..110968, 111117..>111182))	/locus-tag="An14g05570"
CDS	complement(join(109706. .110389,110813..110968, 111117..111182))	/locus-tag="An14g05570"
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exon	complement(111117..1111 82)	/locus-tag="An14g05570"
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mRNA	join(<113124..113934, 113983..>114242)	/locus-tag="An14g05590"
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mRNA            complement(join(<114314     /locus-tag="An14g05600"
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CDS             complement(join(114314.     /locus-tag="An14g05600"
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                                   VPDILSIISLAPRMGCTPESMDPVTGVCLVEAAL
                                   RTTRHCQTAVARPLKYDIPLSLSR
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               118734..118997)

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                                         Aspergillus niger"
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                                         YEDDPFYEDDQDIRRQEISLDYQLLDKFPDFWFL
                                         RHPLHLDVIVSIVCNGSKACIRDK
                                         GNTVSRNLDRGILYQPSLATPRHEIIGSLRTPLD
                                         DEESIAPSWSWVSNPNPVKWGGET
```

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                                                   NNFDPLFMCQSKIASINMKTNLNPYGQYVADVRF
                                                   DWTHDSSEAQTHSTEKEKDILNML
                                                   SMVLILRYDGEEEDFMMGLLVLPTNMPSVYRRSG
                                                   LFSCENGQEFWYNIDTPIVALV"
     exon            117920..118177                /locus-tag="An14g05620"
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     intron          118178..118294                /locus-tag="An14g05620"
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     exon            118295..118597                /locus-tag="An14g05620"
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     intron          118598..118733                /locus-tag="An14g05620"
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     exon            118734..118997                /locus-tag="An14g05620"
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     gene            complement(<119272..>12       /locus-tag="An14g05630"
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     mRNA            complement(join(<119272       /locus-tag="An14g05630"
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                     119883..120299,
                     120386..120822,
                     120879..121016,
                     121097..>121189))
     CDS             complement(join(119272.       /locus-tag="An14g05630"
                     .119830,119883..120299,
                     120386..120822,
                     120879..121016,
                     121097..121189))
                                                   /EC-number="6.2.1.12"
                                                   /inference="profile:COGS:COG0318"
                                                   /inference="profile:PFAM:PF00501"
                                                   /note="unnamed protein product;
                                                   Catalytic activity: ATP +
                                                   4-coumarate + CoA = AMP +
                                                   pyrophosphate + 4-coumaroyl-CoA.
                                                   Pathway: flavonoids, stilbene and
                                                   lignin biosynthesis. Remark: the
                                                   phenylpropanoid enzyme
                                                   4-coumarate:coenzyme A ligase
                                                   (4CL) plays a key role in general
                                                   phenylpropanoid metabolism. 4CL is
                                                   related to a larger class of
                                                   prokaryotic and eukaryotic
                                                   adenylate-forming enzymes and
                                                   shares several conserved peptide
                                                   motifs with these enzymes.
                                                   Similarity: belongs to the
                                                   Acyl-CoA synthetases
                                                   (AMP-forming)/AMP-acid ligases II.
                                                   Title: strong similarity to
                                                   4-coumarate-CoA ligase 3 4CL3 -
                                                   Populus balsamifera"
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                                                   YNQARTIVRQLVSGLRAWGVQKGDCVAIHSFNDI
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                                                   IPEHRIRVFDVLGQSVPDGAVSWT
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                                        ELLEHGEQDWVRFDDENLSRTTTAARLFSSGTTG
                                        LPKAAEITHMNLVAQHEFVFEFNP
                                        RPWRVVIAVPLFHAAAAPSSHFGSLKAGHINYVM
                                        RRFDLPLFLQTVEKYQVTEMAIVP
                                        PIAIAIIMHPMSYERGYLRSIRASNLGAAPMDKD
                                        AQKRFQRLLGPGANCTQVWGMTET
                                        CCIATMFRWDEGDETGSVGRLVPNMEAKLVDDNG
                                        TDISDYGVRGELCVRGPAVTPGYF
                                        NNPVANAESFDEQGWFHTGDIAYCDCATQKWYIV
                                        DRKKELIKVRGFQVAPPELEAVLL
                                        AHPLIVDAAVIGLRDVVPGTELPRAYVVRRPETD
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     intron          complement(120300..1203  /locus-tag="An14g05630"
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     exon            complement(120386..1208  /locus-tag="An14g05630"
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     intron          complement(120823..1208  /locus-tag="An14g05630"
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     exon            complement(120879..1210  /locus-tag="An14g05630"
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     intron          complement(121017..1210  /locus-tag="An14g05630"
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     exon            complement(121097..1211  /locus-tag="An14g05630"
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     gene            complement(<121271..>12  /locus-tag="An14g05640"
                     2416)
     mRNA            complement(join(<121271  /locus-tag="An14g05640"
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                     121457..121657,
                     121705..121797,
                     121861..122051,
                     122150..122275,
                     122396..>122416))
     CDS             complement(join(121271.  /locus-tag="An14g05640"
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                     121705..121797,
                     121861..122051,
                     122150..122275,
                     122396..122416))
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                                             /translation="MAVAAVSGRREPPSAMKMTI
                                             QEVGMFEQINLVPVIPGASSVIPV
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                              MAIFTADRIADKRMVCDTQVRSIAVIADRIRADL
                              EDSTSVRTISTVLRSLSGLVLPLS
                              RPTKYESLVLGGAENEGGSEVAGSAVIGDKHGPR
                              TQTATPRPQLPNAAWRVGGLPAGG
                              GLSARLAAIGLSDPFPTTRNTKTRAPPARPVHAN
                              SSIFSGLQVWRSLNGLPHTMPAMC
                              PALESVPLPAPGDVPCWPSRQNDKPYFSIGAGFI
                              QLKL"
exon            complement(121271..1214   /locus-tag="An14g05640"
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                                          /number=1
intron          complement(121410..1214   /locus-tag="An14g05640"
                56)
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exon            complement(121457..1216   /locus-tag="An14g05640"
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intron          complement(121658..1217   /locus-tag="An14g05640"
                04)
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exon            complement(121705..1217   /locus-tag="An14g05640"
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intron          complement(121798..1218   /locus-tag="An14g05640"
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exon            complement(121861..1220   /locus-tag="An14g05640"
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intron          complement(122052..1221   /locus-tag="An14g05640"
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                                          /number=4
exon            complement(122150..1222   /locus-tag="An14g05640"
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intron          complement(122276..1223   /locus-tag="An14g05640"
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exon            complement(122396..1224   /locus-tag="An14g05640"
                16)
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gene            <122711..>127337          /locus-tag="An14g05650"
mRNA            join(<122711..122827,     /locus-tag="An14g05650"
                122948..123005,
                123087..123243,
                123306..123409,
                123871..124023,
                124127..124263,
                124490..124605,
                124682..124801,
                124889..124955,
                125041..125228,
                125358..125490,
                125911..126029,
                126093..126179,
                126273..126578,
                126625..126770,
                126836..127004,
                127202..>127337)
CDS             join(122711..122827,      /locus-tag="An14g05650"
                122948..123005,
                123087..123243,
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                        123871..124023,
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                        124490..124605,
                        124682..124801,
                        124889..124955,
                        125041..125228,
                        125358..125490,
                        125911..126029,
                        126093..126179,
                        126273..126578,
                        126625..126770,
                        126836..127004,
                        127202..127337)
                                                /codon-start=1
                                                /product="hypothetical protein"
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                                                YRPWSPLGLGHNLDVPIFPRWRRTSSRIFFEMAR
                                                PHQPTAKPSGALHNAADRLVPFCT
                                                CLLFAYNLTASCQNAIAGAGSLCDVGASFMIEWA
                                                NIAEYHIGFVPISNIQGVRSVLQG
                                                SPQHRENEMPMSEVPNPKVLWLNPARRRVFHTFN
                                                LKCSTGQQNAKSLLRGLALYMLGV
                                                AKFAGVLPNDDLQTVKQKAMPLLTRMSGMFAKTP
                                                PTSWVGMTGQRCCGHLLAGGSGLG
                                                GKTVRIACKPDVSLAPFFHFVATRRVIRADGSAR
                                                AGYFCYSSRVRYDSGAQTPVVEVK
                                                LVSSLIWRQTEYSMASLLGGSRAGEGSKGKRRRN
                                                VTNWNQSTLSLACPEQVNQAVRLL
                                                RDPVTETLYCCLLRKTADECFVCSREPSSGHGCS
                                                TPLHNTRISRASNTCRDQPLWRLM
                                                NTGDQVIRLNGWWHGRPITHKWKISTVREVGNGT
                                                IDRGGRATEIIMVSTSFDHFHPGC
                                                LTCKSRVKACRVVFGGHLVVTLSDFRGAFQLPIS
                                                HYYITTSSYIAQEPIPPPALPLLL
                                                HPVLLALPSLPNMVALSTLYNTQYLGHSTHYHSL
                                                FSPSHSRPATTWRVSLSYGSSIRW
                                                QSTNQIESEDRRRVSERHILFFTAGFPSFLADGV
                                                HDSWLYSPEAPDSAGVPEWTGVGA
                                                FGWRPVAYAGLCVSGLSGVRRISPSPSPYRLAIP
                                                PFPLSSTRPQIYLVSVDDAGFGSD
                                                LDGSIAQYPHRRLRIYFQEARSTVAQAILA"
     exon            122711..122827              /locus-tag="An14g05650"
                                                /number=1
     intron          122828..122947              /locus-tag="An14g05650"
                                                /number=1
     exon            122948..123005              /locus-tag="An14g05650"
                                                /number=2
     intron          123006..123086              /locus-tag="An14g05650"
                                                /number=2
     exon            123087..123243              /locus-tag="An14g05650"
                                                /number=3
     intron          123244..123305              /locus-tag="An14g05650"
                                                /number=3
     exon            123306..123409              /locus-tag="An14g05650"
                                                /number=4
     intron          123410..123870              /locus-tag="An14g05650"
                                                /number=4
     exon            123871..124023              /locus-tag="An14g05650"
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intron          124024..124126                  /locus-tag="An14g05650"
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intron          124264..124489                  /locus-tag="An14g05650"
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exon            124490..124605                  /locus-tag="An14g05650"
                                                /number=7
intron          124606..124681                  /locus-tag="An14g05650"
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exon            124682..124801                  /locus-tag="An14g05650"
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exon            126625..126770                  /locus-tag="An14g05650"
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intron          126771..126835                  /locus-tag="An14g05650"
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intron          127005..127201                  /locus-tag="An14g05650"
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exon            127202..127337                  /locus-tag="An14g05650"
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gene            <127622..>128417                /locus-tag="An14g05660"
mRNA            join(<127622..127779,           /locus-tag="An14g05660"
                128125..128227,
                128313..>128417)
CDS             join(127622..127779,            /locus-tag="An14g05660"
                128125..128227,
                128313..128417)

                                                /note="unnamed protein product;
                                                Title: questionable ORF"
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                                                /translation="MPRELGCGEVYGMGDMPTVR
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                                             ELELPSLGRAERGIFTPLESGQMY
                                             QNKRIRILPFASRSVDRAA"
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exon            128313..128417               /locus-tag="An14g05660"
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mRNA            join(<128987..130216,        /locus-tag="An14g05670"
                130286..>130729)
CDS             join(128987..130216,         /locus-tag="An14g05670"
                130286..130729)
                                             /inference="profile:PFAM:PF00172"
                                             /inference="similar to AA
                                             sequence:UniProtKB:AB035491.1"
                                             /note="unnamed protein product;
                                             Remark: the Japanese pear
                                             pathotype of Alternaria alternata
                                             produces host-specific AK-toxin
                                             and causes black spot of Japanese
                                             pear. Transformation of the wild
                                             type with AKTR-1- and
                                             AKT3-1-targeting vectors produced
                                             toxin-deficient (Tox-),
                                             nonpathogenic mutants. Title:
                                             similarity to AK-toxin regulating
                                             protein AktR-1 - Alternaria
                                             alternata"
                                             /citation=[74]
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                                             GGTTWALPTYPFDTPSTADEVNDVSGSSWSPETP
                                             TNAELAFQTVNESTMFPMQDVSLM
                                             NSPPWQEDLHERPETLGLEEFFSGSLDSCSPAMY
                                             IPPTMGSSPVTMVPPTPATLPGDS
                                             YATGGGLSMSSVSPGYFDNFWPDNMASTDEDHET
                                             WRFGTYTDSRSGSGFGQNFLPKTS
                                             HHSPGDIGDLYQELFSLLREYPGLALQRQFYSPF
                                             LHHELQGYAMQSLGQPISTTLSSI
                                             SSYASYLEACDTFDLSMHDGERLAAAEGCVVALH
                                             AVCVQQILSIFGDNFATTGFSKLP
                                             NFAGDQGHTETPVDILLRMTQRVYKLHEDVLRTP
                                             HEDETDWRRWKFAESLRRNIFFAN
                                             IIRTLAGRARRYNGINIDPLDSAILLQLPLPAPE
                                             EMWRARSEGEWMIARAQTQRSWAR
                                             GVDGSMLPALRTLQQLLVLEEVGSVSVTLLLPIT
                                             RMILACAKLNGASYG"
exon            128987..130216               /locus-tag="An14g05670"
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intron          130217..130285               /locus-tag="An14g05670"
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mRNA            join(<131085..131323,   /locus-tag="An14g05680"
                131388..131502,
                131555..131602,
                131645..>131662)
CDS             join(131085..131323,    /locus-tag="An14g05680"
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                131555..131602,
                131645..131662)
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                                        GGFFVPLVSIAAISSEDELVNISWVVDWSRRVPL
                                        FSY"
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intron          131324..131387          /locus-tag="An14g05680"
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exon            131388..131502          /locus-tag="An14g05680"
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intron          131503..131554          /locus-tag="An14g05680"
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exon            131555..131602          /locus-tag="An14g05680"
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intron          131603..131644          /locus-tag="An14g05680"
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gene            <134201..>135346        /locus-tag="An14g05690"
mRNA            join(<134201..134238,   /locus-tag="An14g05690"
                134452..134502,
                134768..134993,
                135113..>135346)
CDS             join(134201..134238,    /locus-tag="An14g05690"
                134452..134502,
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                135113..135346)
                                        /note="unnamed protein product;
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                                        YYEDLPNVADDYLEGASFPHHKPSHVCPESFYNL
                                        FVQYKLDETGRKEGWRPMDRDKNQ
                                        IRADGSATCYECVRDNRGYDSLGKISDSLSLMEK
                                        RIVDPFDRNTPRGVEIIIEGKAML
                                        FIGTFISLFHILITLYDSTFAS"
exon            134201..134238          /locus-tag="An14g05690"
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exon            134452..134502          /locus-tag="An14g05690"
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		/number=3
intron	134994..135112	/locus-tag="An14g05690"
		/number=3
exon	135113..135346	/locus-tag="An14g05690"
		/number=4
gene	complement(<135466..>13 6476)	/locus-tag="An14g05700"
mRNA	complement(join(<135466 ..135580, 135676..135753, 136059..136189, 136290..136364, 136405..>136476))	/locus-tag="An14g05700"
CDS	complement(join(135466. .135580,135676..135753, 136059..136189, 136290..136364, 136405..136476))	/locus-tag="An14g05700"
		/note="unnamed protein product; Title: strong similarity to hypothetical protein encoded by An01g10130 - Aspergillus niger"
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		/protein-id="CAK42131.1"
		/db-xref="GI:134081876"
		/translation="MPMKDSRQLTCRLNSWIRLQ LEYRAGIYYSDTLTRKKPIVPSGT KPRCNRYLVQHYLYGIKRSCPARNSGSKCSGCTD AHDFMDARMENAKELQKVLDSCPS RIEGSWIIPDIHTSAMSATEDDSGVMTGLGVLSG CTLAAFKDRANWNDDDGIPG"
exon	complement(135466..1355 80)	/locus-tag="An14g05700"
		/number=1
intron	complement(135581..1356 75)	/locus-tag="An14g05700"
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exon	complement(135676..1357 53)	/locus-tag="An14g05700"
		/number=2
intron	complement(135754..1360 58)	/locus-tag="An14g05700"
		/number=2
exon	complement(136059..1361 89)	/locus-tag="An14g05700"
		/number=3
intron	complement(136190..1362 89)	/locus-tag="An14g05700"
		/number=3
exon	complement(136290..1363 64)	/locus-tag="An14g05700"
		/number=4
intron	complement(136365..1364 04)	/locus-tag="An14g05700"
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exon	complement(136405..1364 76)	/locus-tag="An14g05700"
		/number=5

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                8530)
mRNA            complement(join(<137703  /locus-tag="An14g05710"
                ..137767,
                137825..137999,
                138078..138298,
                138437..>138530))
CDS             complement(join(137703.  /locus-tag="An14g05710"
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                138078..138298,
                138437..138530))
                                         /inference="profile:COGS:COG0553"
                                         /note="unnamed protein product;
                                         Similarity: although the
                                         similarity to Rhp16 of S. pombe is
                                         weak, some motifs in the predicted
                                         ORF suggest that it might be
                                         involved in DNA binding and
                                         repair. Title: weak similarity to
                                         RAD16 nucleotide excision repair
                                         protein homolog rhp16p -
                                         Schizosaccharomyces pombe"
                                         /citation=[32]
                                         /citation=[61]
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                                         /db-xref="GI:134081877"
                                         /translation="MARYDFYMMSAMFLGSWHTG
                                         SWPRQCEHLGAAGKIKRKRAGPCN
                                         IRDINQPKIKGMRVSTILRFWQPVAIYAIKEFSK
                                         NPMLCCCVLADVMGRGKTWTLTGY
                                         LVDHATYEPDKPTLIICPPHLVWQWASEIKKFTS
                                         KLKILVYFGDAREEPPVPVQALKT
                                         LSSRISDRLHLTQGDIILDTAWWS"
exon            complement(137703..1377  /locus-tag="An14g05710"
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intron          complement(137768..1378  /locus-tag="An14g05710"
                24)
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exon            complement(137825..1379  /locus-tag="An14g05710"
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intron          complement(138000..1380  /locus-tag="An14g05710"
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exon            complement(138078..1382  /locus-tag="An14g05710"
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intron          complement(138299..1384  /locus-tag="An14g05710"
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                                         /number=3
exon            complement(138437..1385  /locus-tag="An14g05710"
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gene            <139122..>140458         /locus-tag="An14g05720"
mRNA            join(<139122..139252,    /locus-tag="An14g05720"
                139343..139427,
                139649..139772,
                139813..139963,
                140010..140120,
                140192..140244,
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                    140337..>140458)
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                    139649..139772,
                    139813..139963,
                    140010..140120,
                    140192..140244,
                    140337..140458)
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                                            /translation="MPYFAVKGKGNSFVDESQGL
                                            APVPSAYRSDKCDMMHAILDLNQR
                                            TCSTHQPRPSTRAVRVPSWFHRTSHEAVEYNITV
                                            TAATSTVSGSFRSLGAHPILILRQ
                                            YDALQGHILYDRGSGQLTSMQACYSRARRHPTSP
                                            IDNHHTAHNEEKGDITLPIDDIFN
                                            YQNTLYLHPLTLVLIGVARHYGENSGQVFLRRQF
                                            HRARKERKWDDGEKSRKMGWMWEE
                                            VELVSWRNGMEGFRGESAKSMYALARWIIRLHRF
                                            MARHLY"
exon                139122..139252          /locus-tag="An14g05720"
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intron              139253..139342          /locus-tag="An14g05720"
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exon                139343..139427          /locus-tag="An14g05720"
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intron              139428..139648          /locus-tag="An14g05720"
                                            /number=2
exon                139649..139772          /locus-tag="An14g05720"
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intron              139773..139812          /locus-tag="An14g05720"
                                            /number=3
exon                139813..139963          /locus-tag="An14g05720"
                                            /number=4
intron              139964..140009          /locus-tag="An14g05720"
                                            /number=4
exon                140010..140120          /locus-tag="An14g05720"
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intron              140121..140191          /locus-tag="An14g05720"
                                            /number=5
exon                140192..140244          /locus-tag="An14g05720"
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intron              140245..140336          /locus-tag="An14g05720"
                                            /number=6
exon                140337..140458          /locus-tag="An14g05720"
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gene                complement(<140647..>14 /locus-tag="An14g05730"
                    2006)
mRNA                complement(join(<140647 /locus-tag="An14g05730"
                    ..141004,
                    141055..141527,
                    141590..141657,
                    141707..141743,
                    141796..141815,
                    141865..141876,
                    141952..>142006))
CDS                 complement(join(140647. /locus-tag="An14g05730"
                    .141004,141055..141527,
                    141590..141657,
                    141707..141743,
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                  141796..141815,
                  141865..141876,
                  141952..142006))
                                       /inference="similar to AA
                                       sequence:UniProtKB:AF119672.1"
                                       /note="unnamed protein product;
                                       Function: PTH11 of M. grisea is
                                       required for appressorium
                                       differentiation in response to
                                       inductive surface cues. Function:
                                       as do most fungal plant pathogens,
                                       M. grisea differentiates an
                                       infection structure specialized
                                       for host penetration called the
                                       appressorium. Phenotype: M. grisea
                                       cells null mutant for PTH11 are no
                                       more pathogenic. Similarity: the
                                       length of the predicted ORF is
                                       only one half of the M. grisea
                                       PTH11. Title: similarity to
                                       integral membrane protein PTH11 -
                                       Magnaporthe grisea"
                                       /citation=[63]
                                       /codon-start=1
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                                       /translation="MTVSHPKDVLNTINFVTQCV
                                       EDWSCLTAWVLFMGYCGIAIAVGH
                                       YGGGYHIDDVSEAHQVLFRKFCYIATVLYCPMAL
                                       FVKIALLSILIRIFNPYRSKIYFI
                                       YGLLGCLCIYYIVAEIVKIRMCDPVPAYWTQDPK
                                       ARCLNQRAALIADSVISVVTDFII
                                       LILPLPLTWSLQMSRNKKLRVIGMLSAGGLATAF
                                       SLYRLVLVLRDGSSRDQTIVFMIV
                                       ILSGNAEGGVAMICACLPTVNILINKLRKKEYSS
                                       QRYYEPESSVNLSKLKGSNKRFSL
                                       GNSRRADGTESASDQSHLITFAGTVDMAGGNDTG
                                       GIHKTVDVSQTIEMVADGDSHESH HHGSFH"
exon              complement(140647..1410  /locus-tag="An14g05730"
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intron            complement(141005..1410  /locus-tag="An14g05730"
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exon              complement(141055..1415  /locus-tag="An14g05730"
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intron            complement(141528..1415  /locus-tag="An14g05730"
                  89)
                                       /number=2
exon              complement(141590..1416  /locus-tag="An14g05730"
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intron            complement(141658..1417  /locus-tag="An14g05730"
                  06)
                                       /number=3
exon              complement(141707..1417  /locus-tag="An14g05730"
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intron            complement(141744..1417  /locus-tag="An14g05730"
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intron	complement(141816..1418 64)	/locus-tag="An14g05730"
		/number=5
exon	complement(141865..1418 76)	/locus-tag="An14g05730"
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intron	complement(141877..1419 51)	/locus-tag="An14g05730"
		/number=6
exon	complement(141952..1420 06)	/locus-tag="An14g05730"
		/number=7
gene	complement(<142716..>14 3896)	/locus-tag="An14g05740"
mRNA	complement(join(<142716 ..142868, 142941..143171, 143244..143322, 143423..143759, 143845..>143896))	/locus-tag="An14g05740"
CDS	complement(join(142716. .142868,142941..143171, 143244..143322, 143423..143759, 143845..143896))	/locus-tag="An14g05740"
		/codon-start=1
		/product="hypothetical protein"
		/protein-id="CAK42135.1"
		/db-xref="GI:134081880"
		/translation="MEEELSGLTRAVVRQQTDPL PNEGDRWSLTGCWNPTRVSRTREI GWEGRAEPWEVEVYPRSLHRTTDYTQLQFSHRLP RVSFFPVDPLYNMQRVANRVGFKP FCSLADRAQGRRLLEAQESFNSSHLRQRDGSHPT LHSTHSKRKSKFFIAALGVYNNPR QGQQRAGQACELRGSILPGLTGSMTVCRSPRHHR LFTDAASQPTFQRSPLCRIPYCGL ARTRRSLIPHSGPWRVVRGAIGTSARGGSNNRRW LLLLVISIVRSRYFRRPAAMSPRL ARRGGGI"
exon	complement(142716..1428 68)	/locus-tag="An14g05740"
		/number=1
intron	complement(142869..1429 40)	/locus-tag="An14g05740"
		/number=1
exon	complement(142941..1431 71)	/locus-tag="An14g05740"
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intron	complement(143172..1432 43)	/locus-tag="An14g05740"
		/number=2
exon	complement(143244..1433 22)	/locus-tag="An14g05740"
		/number=3
intron	complement(143323..1434 22)	/locus-tag="An14g05740"
		/number=3
exon	complement(143423..1437 59)	/locus-tag="An14g05740"

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intron          complement(143760..1438   /locus-tag="An14g05740"
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exon            complement(143845..1438   /locus-tag="An14g05740"
                96)
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gene            <143978..>145355          /locus-tag="An14g05750"
mRNA            join(<143978..144235,     /locus-tag="An14g05750"
                144298..144933,
                144984..>145355)
CDS             join(143978..144235,      /locus-tag="An14g05750"
                144298..144933,
                144984..145355)
                                     /EC-number="1.3.1.42"
                                     /inference="profile:COGS:COG1902"
                                     /inference="profile:PFAM:PF00724"
                                     /inference="similar to AA
                                     sequence:UniProtKB:AF293653.1"
                                     /note="unnamed protein product;
                                     Catalytic activity: OPR3 of A.
                                     thaliana catalyzes the reaction:
                                     8-[(1R,2R)-3-Oxo-2-{(Z)-pent-2-eny
                                     l}cyclopentyl]octanoate + NADP+ =
                                     (15Z)-12-Oxophyto-10,15-dienoate +
                                     NADPH. Phenotype: A. thaliana ORP3
                                     null mutants are male-sterile due
                                     to defects in pollen release
                                     caused by a delay in the stomium
                                     degeneration program. Remark:
                                     Jasmonic acid (JA) and its
                                     precursor 12-oxophytodienoic acid
                                     (OPDA) act as plant growth
                                     regulators and mediate responses
                                     to environmental cues. Title:
                                     strong similarity to
                                     12-oxo-phytodienoate reductase
                                     OPR3 - Arabidopsis thaliana"
                                     /citation=[71]
                                     /citation=[75]
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                                     /protein-id="CAK42136.1"
                                     /db-xref="GI:134081881"
                                     /db-xref="GOA:A2R3W8"
                                     /translation="MTIVQAQGADSKLFQPLAIA
                                     NGKLTLSHRVVHAPLTRNRGEPLN
                                     SNSTPENPNRIWYPGDLVVEYYRQRATPGGLIIS
                                     EGIPPSLESNGMPGVSGLFTEEQA
                                     AGWKRVVDTVHAQGGYIYCQLWHAGRATVPQMTG
                                     YPPVSASASVWDDPEERYTHPAVG
                                     DSEPVRYSDHPPIELTVAHIKQTIQDYCKAAKTA
                                     MDIGFDGVELHSGNGYLPEQFLSS
                                     NINRRTDDYGGTPEKRCRFVLELMDELAQTVGQE
                                     NLAIRLTPFGLYNQARGEQRVETW
                                     TYLCESLKQAHPHLSYVSFVEPRYEQIHSYEEKD
                                     AFLRSWGLSSVDLSSFRKIFGSTP
                                     FFSAGGWDQTNSWGVLEAGKYDALLYGRYFTSNP
                                     DLVERLRKGIPFAPYDRTRFYGPF
                                     EDSAFHYVDYEPAPQNSTGQESVNVSVRL"
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intron          144236..144297            /locus-tag="An14g05750"
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exon              144298..144933                /locus-tag="An14g05750"
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intron            144934..144983                /locus-tag="An14g05750"
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exon              144984..145355                /locus-tag="An14g05750"
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gene              complement(<145510..>14       /locus-tag="An14g05760"
                  6577)
mRNA              complement(join(<145510       /locus-tag="An14g05760"
                  ..145699,
                  145751..145803,
                  145854..145876,
                  145933..146045,
                  146099..146459,
                  146529..>146577))
CDS               complement(join(145510.       /locus-tag="An14g05760"
                  .145699,145751..145803,
                  145854..145876,
                  145933..146045,
                  146099..146459,
                  146529..146577))
                                                /EC-number="1.1.1.245"
                                                /inference="profile:COGS:COG1028"
                                                /inference="profile:PFAM:PF00106"
                                                /note="unnamed protein product;
                                                Catalytic activity: chnA of
                                                Acinetobacter catalyzes the
                                                reaction: Cyclohexanol + NAD+ <=>
                                                Cyclohexanone + NADH. Similarity:
                                                the gene model structure is
                                                confirmed by A. niger EST
                                                EMBLEST:BE759160, which covers
                                                exons 1 to 3. Title: strong
                                                similarity to cyclohexanol
                                                dehydrogenase chnA - Acinetobacter
                                                sp"
                                                /citation=[72]
                                                /codon-start=1
                                                /protein-id="CAK42137.1"
                                                /db-xref="GI:134081882"
                                                /db-xref="GOA:A2R3W9"
                                                /translation="MACKVSGTAFITGGGNGIGK
                                                TTAFALAQNGIEAVSLLDVNESLL
                                                QRTKDELATSHPQVAVELTVGDVSKEACVDEAVR
                                                RTVERFGRIDISVHCAGIVGQPSA
                                                THELTAAEWQRVIDINQTGVLLCQKAVIRQMLTQ
                                                ESRGLRLGRGTIVNVASMFGVVAP
                                                GGWSGLSAYTASKHAVVAFSKMDAKAYIQQEIRI
                                                NAICPGYTDTDMIRTYWDAGYMVP
                                                DSQRVAIGRRAQPEEIADAVLFLASPMSSYMVGS
                                                ALVVDGGYTA"
exon              complement(145510..1456       /locus-tag="An14g05760"
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                  50)
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exon              complement(145751..1458       /locus-tag="An14g05760"
                  03)
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intron            complement(145804..1458       /locus-tag="An14g05760"
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exon            complement(145854..1458  /locus-tag="An14g05760"
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intron          complement(145877..1459  /locus-tag="An14g05760"
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exon            complement(145933..1460  /locus-tag="An14g05760"
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intron          complement(146046..1460  /locus-tag="An14g05760"
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exon            complement(146099..1464  /locus-tag="An14g05760"
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exon            complement(146529..1465  /locus-tag="An14g05760"
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gene            complement(<147404..>14  /locus-tag="An14g05765"
                7784)
mRNA            complement(<147404..>14  /locus-tag="An14g05765"
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CDS             complement(147404..1477  /locus-tag="An14g05765"
                84)
                                                 /note="unnamed protein product;
                                                 Title: strong similarity to EST
                                                 an-3120 -Aspergillus niger"
                                                 /codon-start=1
                                                 /protein-id="CAK42138.1"
                                                 /db-xref="GI:134081883"
                                                 /translation="MSIGKIIGKIIIIPILVIIF
                                                 ICVCIYFLIKHRRDRKRERREDNL
                                                 RAQYYRQQFQQQYMYPHTQMQPQQQQQQPGTPAP
                                                 PYYNHAYAVGQQPVAMNEGEYGYS
                                                 ESMMKKPEPVVYPVQQQHPGSEVV"
exon            complement(147404..1477  /locus-tag="An14g05765"
                84)
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mRNA            join(<149275..150089,    /locus-tag="An14g05780"
                150140..150471,
                150521..>150765)
CDS             join(149275..150089,     /locus-tag="An14g05780"
                150140..150471,
                150521..150765)
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                                                 /inference="profile:PFAM:PF01222"
                                                 /inference="similar to AA
                                                 sequence:PIR:S64014"
                                                 /note="unnamed protein product;
                                                 Function: the S. cerevisiae ERG4
                                                 gene encodes sterol C-24(28)
                                                 reductase which catalyzes the
                                                 final step in the biosynthesis of
                                                 ergosterol. Remark: ergosterol is
                                                 the precursor of vitamin D2.
                                                 Title: strong similarity to sterol
```

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                              C-24 reductase Erg4 -
                              Saccharomyces cerevisiae
                              endoplasmatic reticulum"
                              /citation=[6]
                              /citation=[18]
                              /citation=[22]
                              /citation=[54]
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                              /db-xref="GI:134081884"
                              /db-xref="GOA:A2R3X1"
                              /translation="MKQSKDRSPEGTSNAHEDEK
                              PTFEFGGAPGVTMLMLGFPLLMYY
                              MFIGATLYDGHLPLPDENQSITDFLSHLVDLAHT
                              HAYPNRKAWIIYWTFLVLEGLGYL
                              YLPGVYGKGKCLPHLNGKQLDYYCSAASSWYVTI
                              AAALVLHFSGIFRLSTLVEEFGPL
                              MSVAICSGFLVSIIAYVSALLRGAQHRMTGSHVY
                              DFFMGAELNPRLFQWLDMKMFFEV
                              RIPWYILFLLTLGTALKQWEDYGFVSGEVSFLLL
                              AHFLYANACAKGEELIITSWDMYY
                              EKWGFMLIFWNLAGVPMSYCHCTLYLASHDPSTY
                              KWNPIALGVLFVMYIFAYWVWDTC
                              NSQKNLFRAQERGKPVNRKTFPQLPWKSVKNPVC
                              IKTKTGDSILCSGWYGMARKVHYS
                              CDWFFAFSWGLITGFNSPFPWFYSCFFTVMIIHR
                              ALRDIERCRERYGEAWREYERRVP
                              YLFIPVSRLELVL"
exon          149275..150089      /locus-tag="An14g05780"
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intron        150090..150139      /locus-tag="An14g05780"
                                  /number=1
exon          150140..150471      /locus-tag="An14g05780"
                                  /number=2
intron        150472..150520      /locus-tag="An14g05780"
                                  /number=2
exon          150521..150765      /locus-tag="An14g05780"
                                  /number=3
gene          complement(<151141..>15 /locus-tag="An14g05790"
              3445)
mRNA          complement(join(<151141 /locus-tag="An14g05790"
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              151613..151848,
              151899..152339,
              152378..152673,
              152720..153109,
              153190..153256,
              153395..>153445))
CDS           complement(join(151141. /locus-tag="An14g05790"
              .151564,151613..151848,
              151899..152339,
              152378..152673,
              152720..153109,
              153190..153256,
              153395..153445))
                                  /inference="profile:PFAM:PF04082"
                                  /note="unnamed protein product;
                                  Similarity: the predicted protein
                                  shows similarity to several
                                  putative and described fungal
                                  transcription factors; their
```

common feature is the presence of
a typical binuclear cluster
zinc-finger, responsible for DNA
binding,which is not well
conserved in the predicted
protein. Title: weak similarity to
transcription activator prnA -
Aspergillus nidulans"
/citation=[51]
/codon-start=1
/protein-id="CAK42140.1"
/db-xref="GI:134081885"
/translation="MAARTPSIARNSFRARAIKC
DKVVPCSSCSALGIACGPTGLTEV
SEQRFSAIQEQLATIQQALHQITKPSTSVQPDSH
PIATGPTAPPFEGQSSFHHETLVA
RDAAYSAANTARDGQVGDYVSAALSSLKSSLDRH
NHAMNRSGAQSPAQLNQTLLPVDL
VVAVVKKVKSQPPFFLVSQSWLDSTRVEHLCQSI
YFPLDPVPPGSLTLFYGILFYVIR
DYLHAGDPDLAHFDLQLSLELCERHFVAGLSKPE
IMFEPTLEKIQALLLGIQVLKAQE
ETDVQRCWTFLSLAFNMCQSIGLHRRSTLEKDEF
AIAEAKRHAFWALYTIDKNISLNI
GVTSHFQDHDIDADLYAPSNDPKYRPWDLMGLVI
VEFANVQGRVYDQLYSTSACRADD
EQRSASIERLSSDLMTVRDKLLAIDVSRGLYADS
LHGMAACADFIAYSVLTVIYRAQT
HPRDVMAVSSQCYASATAALQSHLKCFTYFRGRQ
THKQTEYVNWILLYPSFTPFVIVF
THAITTASTADLALLQDTASSLELIKGLSRGSMH
LYTICDAFVRAAQILVNSQQTLTG
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LSFDPNSDSI"

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intron	complement(151849..1518 98)	/locus-tag="An14g05790"
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exon	complement(151899..1523 39)	/locus-tag="An14g05790"
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intron	complement(152340..1523 77)	/locus-tag="An14g05790"
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exon	complement(152378..1526 73)	/locus-tag="An14g05790"
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intron	complement(152674..1527 19)	/locus-tag="An14g05790"
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exon	complement(152720..1531 09)	/locus-tag="An14g05790"
		/number=5

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                    89)
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exon                complement(153190..1532   /locus-tag="An14g05790"
                    56)
                                              /number=6
intron              complement(153257..1533   /locus-tag="An14g05790"
                    94)
                                              /number=6
exon                complement(153395..1534   /locus-tag="An14g05790"
                    45)
                                              /number=7
gene                <154037..>156562          /gene="aguA"
                                              /locus-tag="An14g05800"
mRNA                <154037..>156562          /gene="aguA"
                                              /locus-tag="An14g05800"
CDS                 154037..156562            /gene="aguA"
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                                              /EC-number="3.2.1.131"
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                                              /inference="profile:PFAM:PF03648"
                                              /inference="similar to AA
                                              sequence:UniProtKB:ANI290451.1"
                                              /note="Function: hydrolysis of
                                              alpha-D-1,2-(4-O-methyl)glucuronos
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                                              hardwood xylans. Gene-ID: aguA"
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                                              RDINVPELDPDGFWLQSEGDTVRILGKDARGALY
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                                              APIRWVNQWDNMDGSIERGYYGGASIFFKDGTVVE
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                                              VNANATLLLPENMKGLSRIADACRPYGVQIGISL
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                                              WQNITDSLYTYVPDMAGYLVKADSEGQPGPDTYN
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                                              LDFDLRVDHKPSMVRDIISGQRFN
                                              RTLGGWAAVVNVGTNRTWLGSHLAMSNLYAYGRL
                                              AWSPTDESEQILEDWTRLTFGQNH
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                                              THYGPNPATQDNNGWGQWTRADHD
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                                                  /inference="profile:PFAM:PF00439"
                                                  /inference="similar to AA
                                                  sequence:PIR:S28051"
                                                  /note="unnamed protein product;
                                                  Complex: GCN5 of S. cerevisiae is
                                                  a component of the SAGA complex,
                                                  which posseses histone acetylation
                                                  function and is important for
                                                  transcription in vivo. Function:
                                                  GCN5 of S. cerevisiae and many
                                                  other organisms acetylates
                                                  histones H3 and H4 non-randomly at
                                                  specific lysines, causing
                                                  chromatin remodelling during
                                                  transcriptional activation.
                                                  Similarity: in the C-terminal part
                                                  of the protein there is a
                                                  bromodomain, which function may be
                                                  to tether type A histone
                                                  acetyltransferase to the chromatin
                                                  during gene activation. Title:
                                                  strong similarity to histone
                                                  acetyltransferase Gcn5 -
                                                  Saccharomyces cerevisiae nucleus"
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                                                  /citation=[23]
                                                  /citation=[29]
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                                                  PKMTKDYIARLVYDHTHLSLAICKMPLEIIGGIT
                                                  FREVRHRRFAEIVFCAASSDQQVK
                                                  GYGAHLMAHLKDYVRATSPVMHFLTYADNYATGY
                                                  FQKQGFTKEITLDKSIWMGYIKDY
                                                  EGGTLMQCSMLPRIRYLEVGRMLLKQKACVLAKL
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                                              RPLSRNHIVHPPPPQWANGIVTLI
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                                              RFLSKIQAHKQAWPFLSPVNKDEV
                                              PDYYNFIESPMDLSTMEERLENDTYSTPKELIND
                                              LKSIFRNCRQYNDATTIYAKSATK
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                                              /inference="profile:PFAM:PF01301"
                                              /inference="similar to AA
                                              sequence:UniProtKB:A00968.1"
                                              /note="unnamed protein product;
                                              Catalytic activity: hydrolysis of
                                              terminal,non-reducing
                                              beta-d-galactose residues in
                                              beta-d-galactosides. Function:
                                              cleaves beta-linked terminal
                                              galactosyl residues from
                                              gangliosides, glycoproteins, and
                                              glycosaminoglycans. Remark:
                                              beta-galactosidase of A. niger has
                                              been already patented under
                                              patentnumber WO9010703 and
                                              WO9716555-A1. Similarity: belongs
                                              to family 35 of glycosyl
                                              hydrolases. Similarity: the
                                              absence of nice BLASTN
                                              alignments,demonstrates that the
                                              predicted ORF is just an homologue
                                              of the already described
                                              beta-galactosidase of A. niger.
                                              Title: strong similarity to
                                              beta-galactosidase lacA -
                                              Aspergillus niger
                                              extracellular/secretion proteins"
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                                          VSGGGFPGWLKRVQGRLKTTDQGY
                                          LDAITPYMQAIGRIIAKAQITNGGPVILFQPENE
                                          YTACVQDEGYTQKEYMAYVEEQYR
                                          KAGIVVPFIVNDADPMGNFAPGTGVGAVDIYSFD
                                          DYPLQWSTAPSNPSNWSSLISPLL
                                          SYNETVHEEQSPTTPFSISEFQGGVPDAWGGVGI
                                          ETSAAYIGPEFERIFYKINYGFRA
                                          AIQNLYMIFGGTNWGNLGHSGGYTSYDVGAAIAE
                                          DRQVIREKYSELKLQSNFLQASSA
                                          YLETHSDNGSYGIYTDATSLAVTRLAGNPTNFYV
                                          VRHGELTSRESTSYKLRVNTSAGN
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                                          TAELFTWKQAGSKSVVVLYGGEDE
                                          LHEFAVPANKGKPTSIEGDGLQVQQINSTTVIQW
                                          AVQPSRRVVHFSDTLEVHLLWRNE
                                          AYNYWVLDLPVPGAIGRHVSRSHTNRSVIVKAGY
                                          LLRTAEIIGTSLYLTGDINTTTTI
                                          ELISAPQPVTSILFNKNRIPTTITSPGRLTGTLT
                                          YHKPNISLPDLTTLDWYYLNTLPE
                                          VHDPTYDDHLWTPCTHTTTANPRNLTTPTSLYAS
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                                          YLLTEGGYAYGHSIWLNNTFLASWPGNPAFLLSN
                                          QTITFPSPLTPGTTYKLTILIDHL
                                          GNDENFPANGEFMKDPRGILDYTLHGRDDKSAIS
                                          WKMTGNFGGESYADLSRGPLNEGA
                                          LFAERKGYHLPGAPTEQWTKRSPFDGLPEDERPG
                                          VGFFATKFDLQIPDGYDVPISVVF
                                          ENSTMAGDGSGPARFRSELFVNGWQFGKYVNHIG
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                                          WAMDEKSFKLDGLRLQANAVVQSGYRKPSLVKGE
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intron             160723..160784        /locus-tag="An14g05820"
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intron             160894..160961        /locus-tag="An14g05820"
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exon               160962..162768        /locus-tag="An14g05820"
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mRNA            complement(<163244..>16 /locus-tag="An14g05830"
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CDS             complement(163244..1650 /locus-tag="An14g05830"
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                                        /note="unnamed protein product;
                                        Function: co-expression of het-e
                                        and het-c lead to cell death.
                                        Function: het-e1 of P. anserina is
                                        responsible for vegetative
                                        incompatibility. Remark: het-e1 of
                                        P. anserina shows also two
                                        sequence motifs, a GTP-binding
                                        domain and a repeated region that
                                        shares similarity with that of the
                                        beta-transducin. Remark: the
                                        reactivity of the HET-E protein
                                        depends on two functional
                                        elements, a GTP-binding domain and
                                        several WD40 repeats. Similarity:
                                        the similarity to het-e1 involves
                                        only the N-terminal half of the
                                        predicted protein. Title:
                                        similarity to beta transducin-like
                                        protein het-e1 - Podospora
                                        anserina"
                                        /citation=[26]
                                        /citation=[44]
                                        /citation=[69]
                                        /citation=[73]
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                                        KRSRKCYVYLSDIPSGYGEVPLDEQAGSSVEPAR
                                        RRRPSKYDGTINGPFARCRWFTRG
                                        WTLQELIAPKDLTFYGSGWNVLGTKASMTALIST
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                                        DYDISRGRVVRVDLGLETRATTRD
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                                        TEYYPSRIWDAENHRLRLSSNDST
                                        SLETWAAVRLHNSSGRAIGVVFHISPHRRPESTS
                                        TFNVHGWICMQTMKPDMTLSQIVD
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                                        TFVSGNGSETLINVTVANRYAPCT
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                          167319..>167516))
CDS                       complement(join(166037.    /locus-tag="An14g05840"
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                                                     sequence:UniProtKB:AF159789.1"
                                                     /note="unnamed protein product;
                                                     Catalytic activity: A. flavus omtB
                                                     converts demethylsterigmatocystin
                                                     (DMST) to sterigmatocystin (ST)
                                                     and
                                                     dihydrodemethylsterigmatocystin
                                                     (DHDMST) to
                                                     dihydrosterigmatocystin (DHST).
                                                     Function: A. flavus omtB is a
                                                     demethylsterigmatocystin
                                                     6-O-methyltransferase involved in
                                                     aflatoxin biosynthesis. Remark:
                                                     aflatoxins are polyketide-derived
                                                     secondary metabolites. Title:
                                                     strong similarity to
                                                     O-methyltransferase omtB -
                                                     Aspergillus flavus"
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                                                     QMTDRLSGAVNDSFDIGMPTLAKV
                                                     PEFLRMTNFQNPSGAVKGALQYAEKTEMSLWDWV
                                                     PTKPGFLDACNTFMEADRGSRPSW
                                                     LEWFPVKERIIDGFHQGESNVLLVDVAGGRGHDL
                                                     VAFESKFSEVQGRLILEDLPHVVA
                                                     EATQHPKIEHVSFDLFQAQPIQGARTYYMKFILH
                                                     DWSDEESRQILSHLAAAMKMGYSK
                                                     LIIEEFVLADKDCAMLPAMWDWEMLIFCNSMERT
                                                     ASQWTKVLDSAGFRVVKFWAPPGD
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                                                   Function: PTH11 of M. grisea is
                                                   required for appressorium
                                                   differentiation in response to
                                                   inductive surface cues. Function:
                                                   as do most fungal plant pathogens,
                                                   M. grisea differentiates an
                                                   infection structure specialized
                                                   for host penetration called the
                                                   appressorium. Phenotype: M. grisea
                                                   cells null mutant for PTH11 are no
                                                   more pathogenic. Similarity: the
                                                   similarity to PTH11 of M. grisea
                                                   is limited to the N-terminal half
                                                   of the predicted ORF. Title:
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                                                   protein PTH11 - Magnaporthe
                                                   grisea"
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                                                   QTASPAKRWFLYIFSIISVAWNVL
                                                   AIVAIMGYCRPAEKIWRPEVPGSCFSLKFQLIAG
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                                            SPERGSNHTSITKTTEIEVHEESKSKGDIENPHF
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                                          Function: PTH11 of M. grisea is
                                          required for appressorium
                                          differentiation in response to
                                          inductive surface cues. Function:
                                          as do most fungal plant pathogens,
                                          M. grisea differentiates an
                                          infection structure specialized
                                          for host penetration called the
                                          appressorium. Phenotype: M. grisea
                                          cells null mutant for PTH11 are no
                                          more pathogenic. Similarity: the
                                          length of the predicted ORF is
                                          only one half of the M. grisea
                                          PTH11. Title: similarity to
                                          integral membrane protein PTH11 -
                                          Magnaporthe grisea"
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     intron        173514..173574         /locus-tag="An14g05870"
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     intron        173640..173697         /locus-tag="An14g05870"
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                  175420..175941,
                  176025..176078,
                  176188..>176514)
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                  176025..176078,
                  176188..176514)
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sequence:UniProtKB:NCB9I2.2"
/note="unnamed protein product;
Similarity: the central part of
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similarity to N. crassa B9I2. 20.
Title: strong similarity to
hypothetical conserved protein
B9I2.20 - Neurospora crassa"
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/db-xref="GI:134081894"
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QRVRILYRDYPQYTTRASMSQMTVDDAWAIQKNI
LQLEFPTTAVKALQFALFRTYGIP
TISSLLLHTSQFSNPATSFKRYADTGALIGQFVT
CPPTSSRARTAIARTKFLHSGYRA
SGRILESDMLYTLSLFATEPIRFVERFEWRAMTE
LERCAIGTYWKSLGDALDISYDEL
PSGKSGFSDGLHFLEELRQWGDHYEEENMRPDHR
NRLVADKTMDVIVYGFPKWHILCD
GFCKEPCADSLNQEVFSDTPNEDGRYYVQIWKGM
PYYVQPTMWNRWGPAAWLTWALGL
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EYVDVLEKEHKGQCPFGGRSDQPE ICLSR"

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exon	175420..175941	/locus-tag="An14g05880" /number=2
intron	175942..176024	/locus-tag="An14g05880" /number=2
exon	176025..176078	/locus-tag="An14g05880" /number=3
intron	176079..176187	/locus-tag="An14g05880" /number=3
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gene	<176803..>178484	/locus-tag="An14g05890"
mRNA	join(<176803..177362, 177419..>178484)	/locus-tag="An14g05890"
CDS	join(176803..177362, 177419..178484)	/locus-tag="An14g05890"

/EC-number="5.2.-.-"
/inference="profile:COGS:COG4716"
/note="unnamed protein product;
Remark: CLA compounds(
cis,trans)-9,11-linoleic acid and
(trans, cis)-10,12-linoleic acid
are recognised nutritional
supplements and effective
inhibitors of epidermal
carcinogenesis and forestomach
neoplasia; furthermore CLA has
also been shown to prevent adverse
effects caused by immune
stimulation in chicks, mice and
rats, and has been shown to
decrease the ratio of low density
lipoprotein cholesterol to high

density lipoprotein cholesterol.
Remark: the linoleate isomerase is
used in a method for producing
conjugated linoleic/linolenic acid
(CLA) from oils such as sunflower
oil, safflower oil, corn
oil,linseed oil, etc. Similarity:
the N-terminal part of the
prediction ORF shows also weak
similarity to some
oxidoreductases. Similarity: the
patented protein, as well as the
predicted ORF, show strong
similarity to the 67 kDa
myosin-crossreactive streptococcal
antigen of Streptococcus pyogenes,
a protein with unknown function,
but involved in the pathogenesis
of streptococcal infections.
Title: strong similarity to
linoleate isomerase protein
sequence PCLA591 from patent
WO9932604-A1 -Lactobacillus
reuteri"
/citation=[19]
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TVLEEFHEFWDTEAVKDHPHTRFLTRHKHGLERI
DAKRASLGLRDRVDLFMLASKSDK
SLGRSRICDHFSNSFFKSYYWMLLSTTFGIKPVH
SAAEFRRYLQHYMHDIHEIHCRRK
LDGGRYNRHESIVSPIAHFLCSRGVDFRFHTTVT
DIITTPSSSEPHRVSAIKAIHENE
PEMTINLGERDIVLVSLGSVMSGSTTGTNTSPPS
LELMDIEKDLDENWLLWLELSTKN
PIFGNAYNFCTRMAESRLESFTVTFSSPEFFNRF
TALTGDKVGSGTFVTLKDTPWLLS
INLPQQPLFPDQPAHVQVLWGYAMYPEREGDYIK
KPMLECSGQEIMEEILKQLNFPVQ
GILDHSITLPCVVPRAAATLLVRLRSDRPPVIPP
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intron	177363..177418	/locus-tag="An14g05890" /number=1
exon	177419..178484	/locus-tag="An14g05890" /number=2
gene	complement(<179356..>18 1260)	/locus-tag="An14g05900"
mRNA	complement(join(<179356 ..179403, 179482..>181260))	/locus-tag="An14g05900"
CDS	complement(join(179356. .179403, 179482..181260))	/locus-tag="An14g05900"

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                                        Similarity: other BLASTP hits are
                                        explained by the relatively high
                                        content of low-complexity regions.
                                        Title: strong similarity to
                                        hypothetical protein B14D6.80 -
                                        Neurospora crassa"
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                                        KPPAWNGESDPIVFTSSAPEPTHNLPVRPAISSR
                                        AVNTISLDDDDAGNSSDTRSNNRP
                                        RKEAIQVSSDQLDFPDVDDLLDVAQRVEANAFSS
                                        RTANLLATLEDRSRGSNGESASRS
                                        SRGRRIQDQSDDIEVEEMPPPRKPQRKAIKVTSE
                                        EKEAKAREREAAKAQREHDRQLEK
                                        ERKQKAKEDKAREKQLAADIAEVNKLKVDKKDST
                                        HEMLIDLASTFTDTSLGNQTSELM
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                                        WEPCALHIRDEEEHVLCLIAAQDF
                                        INMIVAPTTEPRNTINDHVERLKLAYPKSRPIYL
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                                        RQYEDSSARPSTRRKQQQPEPVTPIDSDTVEDAL
                                        LDLQVTHSCLIHHTSSPAESAEWI
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                                        ENRSDAFVKMLQEVNRVTASMAYG
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                                                 /note="unnamed protein product;
                                                 Function: ALG2 of S. cerevisiae is
                                                 involved in N-glycosylation,
                                                 converting
```

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                                      man[3]glcnac-pp-dolichol. Title:
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                                      mannosyltransferase Alg2 -
                                      Saccharomyces cerevisiae"
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                                      EGEEEVFIVDQMPACVPFLKVRKQRILFYCHFPD
                                      QLLARRDEGGSVLQLLKGLYRVPF
                                      DWFEGWAVSASDKVVANSRFTRGVVSGVFGREKV
                                      GDLSVVYPCVDTKAGDGGEGVVKD
                                      GEKLWGGKKILLSVNRFERKKDLALAIRAYHGLG
                                      EEKRKGTRLVVAGGYDNRVQENVQ
                                      YHRELDELATGLGLQTATSKTVISALSIPDSIDV
                                      LFLLSVPTAFRDTLLLQAKLLLYT
                                      PINEHFGIVPVEAMRAGVPVLASNTGGPLETIVE
                                      GETGWLRDAKVDADWTAVMDKVLY
                                      GMKQEELDRMSVAAKERVEKEFSLTAMGEKLEQE
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     intron        complement(182602..1826    /locus-tag="An14g05910"
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                   184472..188524,
                   188581..188756,
                   188813..189136,
                   189281..>189440))
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                   188581..188756,
                   188813..189136,
                   189281..189440))
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                                              /inference="profile:PFAM:PF00225"
                                              /note="unnamed protein product;
                                              Function: kinesins are
                                              microtubule-dependent motor
                                              proteins, involved in organelle
```

transport, in mitosis and meiosis, and in the transport of synaptic vesicles along axons of animal neurons. Similarity: the closest homologues, comprising XCENP-E of X. laevis, are involved in driving congression of chromosomes to the metaphase plate. Similarity: the main feature of the predicted ORF is to contain, in the N-terminal half, several kinesin-like domains, explaining the strong similarity to several different kinesin-like proteins. Similarity: the predicted ORF has just half of the length of XCENP-E of X. laevis; the best homologue, having also a corresponding length, is a N. crassa hypothetical protein. Title: strong similarity to kinesin-related protein XCENP-E – Xenopus laevis"
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RVFAETVDQDGVWDYLSDSVSSFLQGYNVSILAY
GQSGAGKSYTMGTSGPSEQSDPRS
MGIIPRAAQLLFEKLEGPAKPNRNSGTGLRTPSR
YSVGSASSFGKASVEKNWQLKATY
VEIYNEQLRDLLVPESTHQGDRGTVTIREDAKGR
IILTGLHQVNINSYEDLMGALSFG
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VMSPTPKDKRMSMPVDMMSGSDAS
VMVDSKLHFVDLAGSERLKNTGASGERAKEGISI
NAGLAALGKVISQLSSRQAGAHVS
YRDSKLTRLLQDSLGGNAYTYMIACVNPAEFHLS
ETVNTVQYAQRARAIQSKPRIQQI
ADESDKHAVIERLKAEVAFLRQQLRNAEENGRRS
AAPQDRAERQNEREVELQNQLLDT
QESYNALSQRHAKLISEIARDSEHAGETDPNDVV
SLVGKTSVERLKRSQSFAESIEQV
VLEYEKTIQSLESSLSNTRSSLSVTESTLLERET
KCAYVETVNSQLQARIQKLLDRES
STETYLHELEARLDGQSTGEEKQAAIVAELRKEL
SRARESEANCEDYISTLEERLAEA
DQDMELMQREMERLEHVIERQRSLGKLDNLLYEL
DHVQQNGNQKEQSEDELETHVPVP
AKGAYKPRTRATSLSLDVLTEAVETAIPESDEGL
TEPAPEAVHEASVEAEATAETDET
NLKVLESATDRLEAQENGARASRASTPTQTKVVA
DKLETVTQELFDLRMQHESTVSEY
EMLEAKYAEAMKALAEFQRDAADEARHPDEKVQD
LLSTNVESRPVSFLEEGKAPGSND
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PQENHVDTREIDEAKAQEVEQMRR
LLMEHQEGVSIMSQKYAQLQSEHEGTLSLIETLK
AELQRSKNSSPPSTPGFKSPVIRR

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                                   MKESHDAREKQLLAEIEELKSLLKTQEEAAKAQD
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                                   HNAVESLQSSEQELSATLAELDKALASIDAMRSE
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                                   QEELVAKLKHVIDEHKATNAAHLEKIASLEKSHG
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                                   SRVSELEKEIDSHKSLADSFKKDLESLQESHKQE
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                                   DVTAETMAEQIQEIMAQKQHFSDK
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                                   DQHHNRLSVIQQERDQALEDAKVK
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                                   EARIRTIEKHLNAEKQLTATLEEA
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               191652..191691))
                                           /note="unnamed protein product;
                                           Similarity: the similarity to NAB2
                                           of M. musculus is weak, and the
                                           gene structure of the predicted
                                           ORF is questionable. Title: weak
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                                           protein 2 NAB2 - Mus musculus"
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                                           GRPSFSTSHRPLVSTSVQLNIVKR
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     intron          complement(191207..1916 /locus-tag="An14g05930"
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                     193783..193884,
                     193959..193985))
                                           /note="unnamed protein product;
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mRNA	complement(join(<194969 ..195817, 195865..196221, 196455..>196478))	/locus-tag="An14g05950"
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                                               of amino acids of the predicted
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                                               an A. thaliana hypothetical
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                                               LYLKPVPYVGIKGWRRMVLLGIRFQAVPRVREYI
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                198598..198694,
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CDS             complement(join(197258.  /locus-tag="An14g05960"
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                197606..197698,
                197751..197968,
                198017..198238,
                198288..198371,
                198435..198525,
                198598..198694,
                198745..198879))
                                               /EC-number="3.5.3.11"
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                          /inference="profile:COGS:COG0010"
                          /inference="profile:PFAM:PF00491"
                          /note="unnamed protein product;
                          Catalytic activity: H2O + agmatine
                          <=> urea + putrescine. Complex:
                          agmatinase of E. coli is a
                          homodimer of the speB gene
                          product. Function: agmatinase of
                          E. coli is part of the second
                          putrescine biosynthetic pathway;
                          it also represents the only
                          pathway for urea biosynthesis in
                          E. coli as no urease is present.
                          Similarity: the predicted ORF
                          shows much stronger similarity to
                          putative agmatinases of N. crassa
                          and S. pombe. Title: strong
                          similarity to agmatinase speB
                          -Escherichia coli"
                          /citation=[4]
                          /citation=[10]
                          /codon-start=1
                          /protein-id="CAK42157.1"
                          /db-xref="GI:134081902"
                          /db-xref="GOA:A2R3Y9"
                          /translation="MYLSVVSLLALSGIVTAHSS
                          HDQTPLAGPHQRLWYNTLPGDGGT
                          QADSVFSGISTFGRLPYFPCLSSEAERYDIAFIG
                          APFDTGTSYRPGARFGPSGIRQGS
                          RRLNLYGGYNVPLQANPFVSDLRVLDCGDIPVTS
                          YDNAWAIQQIEEGHNSVLMRKPFT
                          DAEKYGLSKAGKTLPRIITLGGDHTITLPLLRSI
                          NRAYGPVTVIHFDSHLDSWKPKVF
                          GGSPSQVAAINHGTYFYHAAMEGLLKNDTNIHAG
                          IRTTLSGPSDYENDGYCGFEIVEA
                          REIDTIGTDGIIKKIRERVGTENPVYLSIDIDTL
                          DPAYAPATGTPETGGWSTRELRTI
                          IRGLDGLNFIGADIVEVAPAYDTNAELSTMAAAD
                          VLYEVLTIMVKKGPLSVGRSDEL"
sig-peptide      complement(198823..1988  /locus-tag="An14g05960"
                 79)
                          /inference="protein
                          motif:SignalP:2.0"
mat-peptide      complement(join(197261.  /locus-tag="An14g05960"
                 .197342,197402..197552,
                 197606..197698,
                 197751..197968,
                 198017..198238,
                 198288..198371,
                 198435..198525,
                 198598..198694,
                 198745..198822))
                          /product="unnamed"
exon             complement(197258..1973  /locus-tag="An14g05960"
                 42)
                          /number=1
intron           complement(197343..1974  /locus-tag="An14g05960"
                 01)
                          /number=1
exon             complement(197402..1975  /locus-tag="An14g05960"
                 52)
                          /number=2
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intron	complement(197553..1976 05)	/locus-tag="An14g05960"
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exon	complement(197606..1976 98)	/locus-tag="An14g05960"
		/number=3
intron	complement(197699..1977 50)	/locus-tag="An14g05960"
		/number=3
exon	complement(197751..1979 68)	/locus-tag="An14g05960"
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intron	complement(197969..1980 16)	/locus-tag="An14g05960"
		/number=4
exon	complement(198017..1982 38)	/locus-tag="An14g05960"
		/number=5
intron	complement(198239..1982 87)	/locus-tag="An14g05960"
		/number=5
exon	complement(198288..1983 71)	/locus-tag="An14g05960"
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intron	complement(198372..1984 34)	/locus-tag="An14g05960"
		/number=6
exon	complement(198435..1985 25)	/locus-tag="An14g05960"
		/number=7
intron	complement(198526..1985 97)	/locus-tag="An14g05960"
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exon	complement(198598..1986 94)	/locus-tag="An14g05960"
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intron	complement(198695..1987 44)	/locus-tag="An14g05960"
		/number=8
exon	complement(198745..1988 79)	/locus-tag="An14g05960"
		/number=9
gene	complement(<199830..>20 1412)	/locus-tag="An14g05970"
mRNA	complement(join(<199830 ..200758, 200827..>201412))	/locus-tag="An14g05970"
CDS	complement(join(199830. .200758, 200827..201412))	/locus-tag="An14g05970"
		/inference="profile:COGS:COG0534"
		/inference="profile:PFAM:PF01554"
		/inference="similar to AA sequence:PIR:T37517"
		/note="unnamed protein product; Title: strong similarity to hypothetical protein SPAC11D3.06 – Schizosaccharomyces pombe"
		/codon-start=1
		/protein-id="CAK42158.1"
		/db-xref="GI:134081903"
		/translation="MYDSLPSYRETSSAHTHEEE

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                                          LVEFFRLLKDSIPVILAYTLQNSLQTTSVLIVGR
                                          TSPENLATTAFSLMFAMVTAWMIA
                                          LGGTTALDTLASSTFTGSSNKHDLGILLQRAFFV
                                          LGLFYVPVAILWTCSEPVFLLLGQ
                                          DPQLSRDSARFLTCLIPGGLGYIYFEAMKKYLQA
                                          QGIMRPGTYVLLITVPFNALLNYL
                                          FCYTFRMGLLGAPFATGISYWLSFALLVLYARFI
                                          AGSECWGGWSRKAFENLGTFARLA
                                          FLGVVHVGTEWWAFEIVALAAGRLGTIPLAAQSV
                                          IMTADQVLNTIPFGVGVATSSRVG
                                          SLLGSRDAAGASRAANTAAWLSMALGGAVLAVLM
                                          GTRHVFAKIFNSDEGVVQLTAEVL
                                          PWVALFQIADGLNGSCGGSLRGMGRQHVGALVNL
                                          ASYYCGALPLGIWLAFNGWGLKGL
                                          WVGQCIALYLVGALEWTIVAFSNWEGEVDKAFQR
                                          MDIHDRLEVGHTTNGATTVV"
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exon	complement(199830..2007 58)	/locus-tag="An14g05970"
		/number=1
intron	complement(200759..2008 26)	/locus-tag="An14g05970"
		/number=1
exon	complement(200827..2014 12)	/locus-tag="An14g05970"
		/number=2
gene	<202677..>204146	/locus-tag="An14g05980"
mRNA	join(<202677..203229, 203273..203374, 203431..>204146)	/locus-tag="An14g05980"
CDS	join(202677..203229, 203273..203374, 203431..204146)	/locus-tag="An14g05980"

/inference="profile:COGS:COG0477"
/inference="similar to AA
sequence:PIR:S61140"
/note="unnamed protein product;
Function: TPO3 of S. cerevisiae is
a vacuolar polyamine transporter,
that controlls the cytoplasmic
spermine content. Phenotype: S.
cerevisiae cells in which TPO3 was
disrupted showed an increased
sensitivity to polyamine toxicity
and a decrease in polyamine uptake
activity and polyamine content in
vacuoles. Phenotype: S. cerevisiae
cells overexpressing TPO3 were
resistant to polyamine toxicity
and showed an increase in
polyamine uptake activity and
polyamine content in vacuoles.
Remark: TPO3 of S. cerevisiae is
also called YPR156c or P9584. 7.
Similarity: the predicted ORF is
125 amino acids longer at the
N-terminus than TPO3 of S.
cerevisiae. Title: strong
similarity to polyamine transport
protein Tpo3 - Saccharomyces
cerevisiae"
/codon-start=1

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                                      /protein-id="CAK42159.1"
                                      /db-xref="GI:134081904"
                                      /translation="MNLKLTQIDLVPVPEKQSAS
                                      DIDSLPVEQHGTHTHPAPTSDPLD
                                      PLNWPRWRKHVILGIVMLKFVLPEQSRRTHRLTM
                                      NRYFLFTYITTTTVPSFAEIQSQY
                                      DINYSQVNWTVAIPALGLSLGPLFWSSVGDIYGR
                                      RIVFIVGTVIALVATIGAAVADTY
                                      GGYMAARFFQGFGVSPSSTVGMAVANGTVTDMFY
                                      EYERGQKLGLWVLALDSGLLLGPT
                                      FGGFLNLVSAQWINWFNAILFAALLLLELTLMPE
                                      TLYPRALMLQRMAVTEKPAESNAG
                                      IEEAGIKRTKSLPFFNLRPIPGLSHPPIYASLTR
                                      FLLTFRFPVIAVAVIGYSFTWYWW
                                      ILSVITMVPSAYATDSPLIQGLLFLGLLIGTLVA
                                      EVSCSGRLSDAIVGRLAKRNGGVR
                                      VPEMRLWLAYPAIVLTAGVYIPIAHVRTISNIAI
                                      QPAVGLILWGISIDKAYHWMVGQV AFFLCE"
exon           202677..203229         /locus-tag="An14g05980"
                                      /number=1
intron         203230..203272         /locus-tag="An14g05980"
                                      /number=1
exon           203273..203374         /locus-tag="An14g05980"
                                      /number=2
intron         203375..203430         /locus-tag="An14g05980"
                                      /number=2
exon           203431..204146         /locus-tag="An14g05980"
                                      /number=3
gene           complement(<205094..>20 /locus-tag="An14g05990"
               7843)
mRNA           complement(join(<205094 /locus-tag="An14g05990"
               ..207273,
               207361..207431,
               207517..207554,
               207700..>207843))
CDS            complement(join(205094. /locus-tag="An14g05990"
               .207273,207361..207431,
               207517..207554,
               207700..207843))
                                      /note="unnamed protein product;
                                      Title: weak similarity to spindle
                                      pole body-associated protein sad1p
                                      - Schizosaccharomyces pombe"
                                      /codon-start=1
                                      /protein-id="CAK42160.1"
                                      /db-xref="GI:134081905"
                                      /translation="MRNLVYPKYHVLESLNRPCD
                                      AVDRHSTRVFSRRVAFALEGRQLP
                                      RIAIDTSELVILVAAIVALASPALDLCLRLQASY
                                      SVPSSHTNRNIKPILLRIELPMPA
                                      RRGATRRAGSTRSDIGSASTYFQSKLGPEARTQA
                                      LPNLPTKQSFAYGSAETPILPREL
                                      KIQPHMDLTEMADAIDKGIEDAKDRQMKEKETTQ
                                      DKSRRQKSPSITRSPVRRSRREPT
                                      PDELQLLDNLREATKSPTPVRGNYSNNDQSTATP
                                      TPPIPHTLSTASSPAQSLPVPRYP
                                      HVPAENLYPSPMGRFGPQLHDGPPLGSSPLPDDS
                                      SLYSFTVERAINSDELTRTLSDGK
                                      NIKAPPRRFSGLAFANEPIHEEEEPDSRLLKTKS
                                      RSPSLQPSYEDFQIEPSPEPEPQS
                                      EPESVQELELEPTPEPEPIPELEPMPEPTPEPEV
                                      IREKSPAAQFTAPTKTLIPNAYAR
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                              RTPSQEPSVDDGQQNIRQTGQSWSWVGSLSAQLP
                              SVSTVARILAGIALAAATVYLVAF
                              GGIPSLSRPPQYIPMDENNMLAVSSLTDQMSRIG
                              AQVSSLAKEMRTVKWDVNEVQSEV
                              RSSPTPIMPPSRGSTDLGPPTEQKTNFLSIGLGV
                              IVIPGLTSPTVGHKLSAWQWAYVN
                              LWRGSHYRPASPPLAALVPWEDYGDCWCSTPRDG
                              MSQIGIDLGQKIVPEEVAVEHMPK
                              TATLKPENAPREMELWAQYVLVQKGTSRPARTQA
                              ERFSIHKPIMDALRSAWPTEDPTA
                              YSDDPLLGPTYYRVGKFTYDIHGSHHVQRFELDA
                              VIDSPEVRVDRVVFRATSNWGGNH
                              TCIYRLKLFGHV"
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exon	complement(205094..2072 73)	/locus-tag="An14g05990"
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intron	complement(207274..2073 60)	/locus-tag="An14g05990"
		/number=1
exon	complement(207361..2074 31)	/locus-tag="An14g05990"
		/number=2
intron	complement(207432..2075 16)	/locus-tag="An14g05990"
		/number=2
exon	complement(207517..2075 54)	/locus-tag="An14g05990"
		/number=3
intron	complement(207555..2076 99)	/locus-tag="An14g05990"
		/number=3
exon	complement(207700..2078 43)	/locus-tag="An14g05990"
		/number=4
gene	complement(<208451..>21 0658)	/locus-tag="An14g06000"
mRNA	complement(join(<208451 ..208726, 208778..209568, 209634..209834, 209889..210489, 210572..>210658))	/locus-tag="An14g06000"
CDS	complement(join(208451. .208726,208778..209568, 209634..209834, 209889..210489, 210572..210658))	/locus-tag="An14g06000"

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                              /inference="profile:COGS:COG5635"
                              /inference="profile:PFAM:PF00400"
                              /inference="similar to AA
                              sequence:PIR:S56893"
                              /note="unnamed protein product;
                              Function: MDV1 of S. cerevisiae is
                              involved in the mitochondrial
                              membrane fission event by
                              regulating the assembly of Dnm1p,
                              a dynamin-related GTPase, into
                              punctate structures at the outer
                              mitochondrial membrane. Phenotype:
                              the mitochondrial fission is
                              blocked in S. cerevisiae MDV null
```

```
                                    mutants and mitochondrial
                                    membranes form nets. Remark: is
                                    also called YJL112w, NET2, FIS2 or
                                    GAG3. Title: strong similarity to
                                    mitochondrial fission protein Mdv1
                                    - Saccharomyces cerevisiae"
                                    /citation=[77]
                                    /citation=[78]
                                    /codon-start=1
                                    /protein-id="CAK42161.1"
                                    /db-xref="GI:134081906"
                                    /translation="MDKHRRRDESPSGLSDIVEP
                                    DGLLGTGITSRHIEAFGRKVTSTA
                                    GHLMGPAPDSSTGGHYHTAMADIQRELRHPNTQR
                                    KVFSLTQTTPTDLVRSKLSTTEIQ
                                    SRAISSLPDELLANIPDDSSSYSLFQGFQASQDD
                                    IEYRRAHRRRSSKSKKLLKDGETR
                                    GALPSAPSDLKKERDLLSRRMELMGVRKNMCSSE
                                    IHDIDNKIANLHNMRKIVLDRLAG
                                    LEMEEADLEHELNEIENKLEDIQEEQQEAEVPPP
                                    ATPKSSEANDDSIVSEDPAMGASF
                                    MSESIYQKIPSPKSVKQRSIILHEHFAPGSEIKE
                                    MPAHSDMVTAIDFDYPFGTMISAA
                                    LDDTVRVWDLNVGRCVGFLEGHNASVRCLQIEDN
                                    IVATGSMDASVKLWDLSRARTTTR
                                    DNRVTRREDDEESAQADDASMASHSTTLEDCYVY
                                    SLDAHVDEVTALHFKGDTLISGSA
                                    DKTLRQWDLVKGRCVQTLDVLWAAAQASTLGSET
                                    TWRPSGRLPDASADFVGAVQCFDA
                                    ALACGTADGMVRLWDLRSGQVHRSLVGHTGPITC
                                    LQFDDVHLVTGSQDRSIRIWDLRT
                                    GSIFDAYAYDKPITSMMFDTKRIVAAAGENVVKV
                                    YDKADGHHWDCGAGVGVDDSGPQP
                                    ATVERVRLKDGFLVEGRKDGIVAAWTC"
    exon            complement(208451..2087   /locus-tag="An14g06000"
                    26)
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    intron          complement(208727..2087   /locus-tag="An14g06000"
                    77)
                                              /number=1
    exon            complement(208778..2095   /locus-tag="An14g06000"
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                                              /number=2
    intron          complement(209569..2096   /locus-tag="An14g06000"
                    33)
                                              /number=2
    exon            complement(209634..2098   /locus-tag="An14g06000"
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                                              /number=3
    intron          complement(209835..2098   /locus-tag="An14g06000"
                    88)
                                              /number=3
    exon            complement(209889..2104   /locus-tag="An14g06000"
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                                              /number=4
    intron          complement(210490..2105   /locus-tag="An14g06000"
                    71)
                                              /number=4
    exon            complement(210572..2106   /locus-tag="An14g06000"
                    58)
                                              /number=5
    gene            <211445..>212528          /locus-tag="An14g06010"
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mRNA	join(<211445..211515, 211743..212394, 212451..>212528)	/locus-tag="An14g06010"
CDS	join(211445..211515, 211743..212394, 212451..212528)	/locus-tag="An14g06010"
		/EC-number="5.4.99.5"
		/inference="profile:COGS:COG1605"
		/inference="profile:PFAM:PF01817"
		/inference="similar to AA sequence:UniProtKB:AF133241.1"
		/note="unnamed protein product; Catalytic activity: chorismate mutases convert chorismate <=> prephenate. Function: aroC of A. nidulans is an allosterically regulated chorismate mutase acting at the first branch point of aromatic amino acid biosynthesis to generate prephenate. Induction: tryptophan acts as heterotropic activator of aroC from A. nidulans. Repression: tyrosine act as negative acting,heterotropic feedback-inhibitor of aroC from A. nidulans. Title: strong similarity to chorismate mutase aroC -Aspergillus nidulans cytoplasm"
		/citation=[60]
		/codon-start=1
		/protein-id="CAK42162.1"
		/db-xref="GI:134081907"
		/db-xref="GOA:A2R3Z4"
		/translation="MDTAIDLSDASKALDLANIR FQLIRLEDTITFHLIERAQFPLNK PIYLSGGVKIPGTDLSLLDYFLREQERLESRVRR YQSPDEYPFFPDSLEEPILAPIKY PKILHDNDVNVNSTLKQRYIEDILPAVCAQFGRE DRGEAQENYGSAATCDVHCLQALS RRIHFGKFVAEAKFQQETERFVKLIKANDRKGID DAITKPEVELKVLERLALKAKTYG TDPGFQPENGPKINVDAVVAMYKEYVIPLTKVVE VDYLMQRLKGTQWE"
exon	211445..211515	/locus-tag="An14g06010" /number=1
intron	211516..211742	/locus-tag="An14g06010" /number=1
exon	211743..212394	/locus-tag="An14g06010" /number=2
intron	212395..212450	/locus-tag="An14g06010" /number=2
exon	212451..212528	/locus-tag="An14g06010" /number=3
gene	complement(<212729..>21 3754)	/locus-tag="An14g06020"
mRNA	complement(join(<212729 ..213283, 213342..213578, 213671..>213754))	/locus-tag="An14g06020"
CDS	complement(join(212729. .213283,213342..213578, 213671..213754))	/locus-tag="An14g06020"

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                                /inference="similar to AA
                                sequence:PIR:T41474"
                                /note="unnamed protein product;
                                Similarity: the ORF shows
                                similarity to putative cdk
                                inhibotor p21 binding protein
                                TOK-1 of H. sapiens. Title: strong
                                similarity to hypothetical cdk
                                inhibitor p21 binding protein
                                SPCC613.08 -Schizosaccharomyces
                                pombe"
                                /codon-start=1
                                /protein-id="CAK42163.1"
                                /db-xref="GI:134081908"
                                /translation="MVKRKELKDNDVEMSGTDPR
                                VDGDDSDEDMDMVNVDFEWFDPQP
                                AVDFHGLKNLLRQLFDTDAQIFDMSALADLILSQ
                                PLLGSTVKVDGNESDPYAFLTVLN
                                LQEHKDKPVIKDLTAYLQRKANAVPTLAPLAQLL
                                SQTPIPPIGLILTERLINMPAEVV
                                PPMYTMLQEEIEWAIKDKEPYNFSHYLIVSKTYE
                                EVESKLDAEESRPQKKKKKAAGGE
                                KAERFLFHPEDEVLERHAVCVGPVEYTHKAEEGL
                                SDAKRAFQDLGIVTKGSLILLEAS
                                KLDGAVKDMAEYFKP"
     exon              complement(212729..2132  /locus-tag="An14g06020"
                       83)
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     intron            complement(213284..2133  /locus-tag="An14g06020"
                       41)
                                                /number=1
     exon              complement(213342..2135  /locus-tag="An14g06020"
                       78)
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     intron            complement(213579..2136  /locus-tag="An14g06020"
                       70)
                                                /number=2
     exon              complement(213671..2137  /locus-tag="An14g06020"
                       54)
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     gene              <214408..>214606         /locus-tag="An14g06030"
     mRNA              join(<214408..214444,    /locus-tag="An14g06030"
                       214506..>214606)
     CDS               join(214408..214444,     /locus-tag="An14g06030"
                       214506..214606)
                                                /note="Remark: the predicted ORF
                                                is only 45 amino acids long."
                                                /codon-start=1
                                                /product="hypothetical protein"
                                                /protein-id="CAK42164.1"
                                                /db-xref="GI:134081909"
                                                /translation="MPFAQNGDAVTKADYQVEEG
                                                IKYLREVKTTLHPFVVKAPSVGSY T"
     exon              214408..214444           /locus-tag="An14g06030"
                                                /number=1
     intron            214445..214505           /locus-tag="An14g06030"
                                                /number=1
     exon              214506..214606           /locus-tag="An14g06030"
                                                /number=2
     gene              complement(<216128..>21  /locus-tag="An14g06040"
                       7084)
     mRNA              complement(<216128..>21  /locus-tag="An14g06040"
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                        7084)
CDS          complement(216128..2170  /locus-tag="An14g06040"
             84)
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                                      /inference="similar to AA
                                      sequence:PIR:T39714"
                                      /note="unnamed protein product;
                                      Similarity: the predcited ORF is
                                      96 amino acids longer at the
                                      N-terminus than the hypothetical
                                      protein SPBC17D11. 03c of S.
                                      pombe. Title: weak similarity to
                                      hypothetical protein SPBC17D11.03c
                                      - Schizosaccharomyces pombe"
                                      /codon-start=1
                                      /protein-id="CAK42165.1"
                                      /db-xref="GI:134081910"
                                      /translation="MARNPSRLLPPSRSLQLTTS
                                      KRQFGTGASILPLLSPPRYRPLRS
                                      SLISSTPSSSPLAHRIPTFATPLRTITTSSNSAP
                                      TKMTTTIDPKYAQLFQSLESQFQT
                                      TTLPHDKWYILAISTLVANPDPERADQLYLYLTS
                                      KPEYSTPSSRQDLIRRIREALIKS
                                      VIIVGVCKPIEAILAISKLEAPEDKDYTFTRENW
                                      QCDEANHERGVAWLEKLYARNTSG
                                      TLDLFAAHKDFAWLSKEITYGLFLSDRGVLDDLD
                                      TQLVVLPAIMSQNLKIETHWHIRG
                                      TRRLGVSLEDVRVLCEGVKHVAGFYGRVLDKVPS
                                      VEEVEGDV"
exon         complement(216128..2170  /locus-tag="An14g06040"
             84)
                                      /number=1
gene         <217593..>218104         /locus-tag="An14g06050"
mRNA         join(<217593..217931,    /locus-tag="An14g06050"
             218003..>218104)
CDS          join(217593..217931,     /locus-tag="An14g06050"
             218003..218104)
                                      /note="unnamed protein product;
                                      Title: weak similarity to
                                      hypothetical protein B10H18.060 -
                                      Neurospora crassa"
                                      /codon-start=1
                                      /protein-id="CAK42166.1"
                                      /db-xref="GI:134081911"
                                      /translation="MSSSGAGQSSVGSRAIYEAG
                                      DQRNVPQSEINEQNRYAEGQKNSH
                                      KNLDSSMPPSSLLPSNHSGDIVLTNTKTEDQRSI
                                      GNKLASQERKPESDHHHNFDQNPE
                                      AELSKQDPTKPAKVHGNEPSKGAKIDAELQAEDE
                                      QRLREKGIKK"
exon         217593..217931           /locus-tag="An14g06050"
                                      /number=1
intron       217932..218002           /locus-tag="An14g06050"
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MOLECULE TYPE (CI):        DNA; circular
DIVISION CODE (CI):        Bacteria
DATE (DATE):               24 Jan 2006
DEFINITION (DEF):          Streptococcus mutans UA159, complete genome.
SOURCE:                    Streptococcus mutans UA159
 ORGANISM (ORGN):          Streptococcus mutans UA159
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     On or before Jan 18, 2006 this sequence version replaced
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REFERENCE:               1  (bases 1 to 2030921)
   AUTHOR (AU):          Ajdic,D.; McShan,W.M.; McLaughlin,R.E.; Savic,G.;
                         Chang,J.; Carson,M.B.; Primeaux,C.; Tian,R.; Kenton,S.;
                         Jia,H.; Lin,S.; Qian,Y.; Li,S.; Zhu,H.; Najar,F.;
                         Lai,H.; White,J.; Roe,B.A.; Ferretti,J.J.
   TITLE (TI):           Genome sequence of Streptococcus mutans UA159, a
                         cariogenic dental pathogen
   JOURNAL (SO):         Proc. Natl. Acad. Sci. U.S.A., 99 (22), 14434-14439
                         (2002)
   OTHER SOURCE (OS):    CA 137:364100
REFERENCE:               2  (bases 1 to 2030921)
   AUTHOR (AU):          Ajdic,D.; McShan,W.M.; McLaughlin,R.E.; Savic,G.;
                         Chang,J.; Carson,M.B.; Primeaux,C.; Tian,R.; Kenton,S.;
                         Jia,H.; Lin,S.; Qian,Y.; Li,S.; Zhu,H.; Najar,F.;
                         Lai,H.; White,J.; Roe,B.A.; Ferretti,J.J.
   TITLE (TI):           Direct Submission
   JOURNAL (SO):         Submitted (09-JUL-2002) Department of Microbiology and
                         Immunology, University of Oklahoma Health Sciences
                         Center, 940 SL Young Blvd., Oklahoma City, OK 73104,
                         USA


FEATURES (FEAT):
   Feature Key      Location              Qualifier
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source           1..2030921            /organism="Streptococcus mutans
                                        UA159"
                                        /mol-type="genomic DNA"
                                        /strain="UA159"
                                        /db-xref="taxon:210007"



L5   ANSWER 27 OF 27      GENBANK®  COPYRIGHT 2008 on STN

LOCUS (LOC):             BX571856     GenBank (R)
GenBank ACC. NO. (GBN):  BX571856
GenBank VERSION (VER):   BX571856.1  GI:49240382
CAS REGISTRY NO. (RN):   726687-34-9
SEQUENCE LENGTH (SQL):   2902619
MOLECULE TYPE (CI):      DNA; circular
DIVISION CODE (CI):      Bacteria
DATE (DATE):             7 Oct 2006
DEFINITION (DEF):        Staphylococcus aureus subsp. aureus strain MRSA252,
                         complete genome.
KEYWORDS (ST):           complete genome
SOURCE:                  Staphylococcus aureus subsp. aureus MRSA252
 ORGANISM (ORGN):        Staphylococcus aureus subsp. aureus MRSA252
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                              Bacteria; Firmicutes; Bacillales; Staphylococcus
REFERENCE:                    1  (bases 1 to 2902619)
   AUTHOR (AU):               Holden,M.T.; Feil,E.J.; Lindsay,J.A.; Peacock,S.J.;
                              Day,N.P.; Enright,M.C.; Foster,T.J.; Moore,C.E.;
                              Hurst,L.; Atkin,R.; Barron,A.; Bason,N.; Bentley,S.D.;
                              Chillingworth,C.; Chillingworth,T.; Churcher,C.;
                              Clark,L.; Corton,C.; Cronin,A.; Doggett,J.; Dowd,L.;
                              Feltwell,T.; Hance,Z.; Harris,B.; Hauser,H.;
                              Holroyd,S.; Jagels,K.; James,K.D.; Lennard,N.; Line,A.;
                              Mayes,R.; Moule,S.; Mungall,K.; Ormond,D.; Quail,M.A.;
                              Rabbinowitsch,E.; Rutherford,K.; Sanders,M.; Sharp,S.;
                              Simmonds,M.; Stevens,K.; Whitehead,S.; Barrell,B.G.;
                              Spratt,B.G.; Parkhill,J.
   TITLE (TI):                Complete genomes of two clinical Staphylococcus aureus
                              strains: evidence for the rapid evolution of virulence
                              and drug resistance
   JOURNAL (SO):              Proc. Natl. Acad. Sci. U.S.A., 101 (26), 9786-9791
                              (2004)
   OTHER SOURCE (OS):         CA 141:152000
REFERENCE:                    2  (bases 1 to 2902619)
   AUTHOR (AU):               Holden,M.T.G.
   TITLE (TI):                Direct Submission
   JOURNAL (SO):              Submitted (23-JUN-2004) Submitted on behalf of the
                              Pathogen Sequencing Unit, Sanger Institute, Wellcome
                              Trust Genome Campus, Hinxton, Cambridge CB10 1SA,
                              E-mail: mh3@sanger.ac.uk


FEATURES (FEAT):
   Feature Key      Location                 Qualifier
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=> d l5 20

L5   ANSWER 20 OF 27  USPATFULL on STN
AN      2003:71519  USPATFULL
TI      Corynebacterium glutamicum genes encoding metabolic pathway proteins
IN      Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF
        Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
        Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF
        Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF
        Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF
        Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF
        Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF
        Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF
PI      US 20030049804     A1  20030313
AI      US 2000-746660     A1  20001222 (9)
RLI     Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,
        PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun
        2000, PENDING
PRAI    DE 1999-19931420     19990708
        US 1999-141031P      19990625 (60)
        US 1999-142101P      19990702 (60)
        US 1999-148613P      19990812 (60)
        US 2000-187970P      20000309 (60)
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DT      Utility
FS      APPLICATION
LN.CNT 15004
INCL    INCLM: 435/115.000
        INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200
NCL     NCLM:  435/115.000
        NCLS:  435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200
IC      [7]
        ICM    C12P013-08
        ICS    C07H021-04; C12N009-00; C12P021-02; C12N001-21
        IPCI   C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
               C07H0021-00 [ICS,7,C*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];
               C12N0001-21 [ICS,7]
        IPCR   C07K0014-195 [I,C*]; C07K0014-34 [I,A]; C12N0001-21 [I,C*];
               C12N0001-21 [I,A]; C12N0009-00 [I,C*]; C12N0009-00 [I,A];
               C12N0009-18 [I,C*]; C12N0009-18 [I,A]; C12N0009-90 [I,C*];
               C12N0009-90 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 21

L5      ANSWER 21 OF 27  USPATFULL on STN
AN      2003:95966  USPATFULL
TI      Polynucleotides, materials incorporating them, and methods for using
        them
IN      Glenn, Matthew, Auckland, NEW ZEALAND
        Havukkala, Ilkka J., Auckland, NEW ZEALAND
        Bloksberg, Leonard N., Auckland, NEW ZEALAND
        Lubbers, Mark W., Palmerston North, NEW ZEALAND
        Dekker, James, Palmerston North, NEW ZEALAND
        Christensson, Anna C., Lund, SWEDEN
        Holland, Ross, Palmerson North, NEW ZEALAND
        O'Toole, Paul W., Palmerston North, NEW ZEALAND
        Reid, Julian R., Palmerston North, NEW ZEALAND
        Coolbear, Timothy, Palmerston North, NEW ZEALAND
PA      Genesis Research & Development Corp. Ltd, Parnell, NEW ZEALAND (non-U.S.
        corporation)
        Via Lachia Bioscience (NZ) Ltd., Auckland, NEW ZEALAND (non-U.S.
        corporation)
PI      US 6544772        B1  20030408
AI      US 2000-634238          20000808 (9)
DT      Utility
FS      GRANTED
LN.CNT 2015
INCL    INCLM: 435/252.300
        INCLS: 435/320.100; 536/023.700
NCL     NCLM:  435/252.300
        NCLS:  435/320.100; 536/023.700
IC      [7]
        ICM    C12N001-21
        ICS    C12N015-63; C12N015-31
        IPCI   C12N0001-21 [ICM,7]; C12N0015-63 [ICS,7]; C12N0015-31 [ICS,7]
        IPCR   A23C0019-00 [I,C*]; A23C0019-032 [I,A]; C07K0014-195 [I,C*];
               C07K0014-335 [I,A]; C12N0001-21 [I,C*]; C12N0001-21 [I,A];
               C12N0015-31 [I,C*]; C12N0015-31 [I,A]
EXF     435/252.3; 435/320.1; 536/23.7
CAS INDEXING IS AVAILABLE FOR THIS PATENT.


=> d l5 22
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```
L5      ANSWER 22 OF 27  BIOTECHDS COPYRIGHT 2008 THOMSON REUTERS on STN
AN      1999-00562  BIOTECHDS
TI      Use of lactic and propionic acid bacteria;
            to bind mycotoxin to prevent their absorption or to purify
            contaminated food or feedstuff
AU      El-Nezami H; Kankaanpaa P; Salminen S; Ahokas J
PA      Roy.Melbourne-Inst.Technol.
LO      Melbourne, Victoria, Australia.
PI      WO 9834503 13 Aug 1998
AI      WO 1998-AU63 6 Feb 1998
PRAI    AU 1997-5005 7 Feb 1997
DT      Patent
LA      English
OS      WPI: 1998-557001 [49]


=> d hist

        (FILE 'HOME' ENTERED AT 13:55:21 ON 07 JUL 2008)

        INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
        AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
        CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
        DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:55:47 ON 07 JUL 2008
                    SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND? AND CD4+ CELL? AND
                ---------
                0*  FILE ADISCTI
                 SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND? AND CD4+ CELLS
                ---------
                0*  FILE ADISCTI
                 SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND?
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                0*  FILE ADISNEWS
                0*  FILE ANTE
                0*  FILE AQUALINE
                0*  FILE BIOENG
                1*  FILE BIOTECHABS
                1*  FILE BIOTECHDS
                0*  FILE BIOTECHNO
                2   FILE CAPLUS
                0*  FILE CEABA-VTB
                0*  FILE CIN
                0*  FILE ESBIOBASE
                0*  FILE FOMAD
                0*  FILE FOREGE
                2*  FILE FROSTI
                0*  FILE FSTA
                5   FILE GENBANK
                1   FILE IFIPAT
                0*  FILE KOSMET
                0*  FILE NTIS
                0*  FILE NUTRACEUT
                1*  FILE PASCAL
                0*  FILE PHARMAML
                1   FILE SCISEARCH
                1   FILE TOXCENTER
               21   FILE USPATFULL
                3   FILE USPAT2
                0*  FILE WATER
                2   FILE WPIDS
                2   FILE WPINDEX
L1              QUE LACTOBACILLUS REUTERI AND TOXIN(P) BIND?
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      FILE 'BIOTECHDS, CAPLUS, FROSTI, GENBANK, IFIPAT, PASCAL, SCISEARCH,
      TOXCENTER, USPATFULL, USPAT2' ENTERED AT 13:59:37 ON 07 JUL 2008
L2              38 S L1
L3              34 DUP REM L2 (4 DUPLICATES REMOVED)
L4              27 S L3 AND (TABLET OR FOOD OR DIETARY SUPLEMENT OR CONFECTIONERY
L5              27 DUP REM L4 (0 DUPLICATES REMOVED)

=> logoff
ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF
LOGOFF? (Y)/N/HOLD:y
COST IN U.S. DOLLARS                                   SINCE FILE      TOTAL
                                                          ENTRY      SESSION
FULL ESTIMATED COST                                      174.83       178.94

STN INTERNATIONAL LOGOFF AT 14:06:30 ON 07 JUL 2008




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Welcome to STN International!  Enter x:x

LOGINID:ssspt189dxw

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2


* * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1             Web Page for STN Seminar Schedule - N. America
 NEWS  2  NOV 21     CAS patent coverage to include exemplified prophetic
                     substances identified in English-, French-, German-,
                     and Japanese-language basic patents from 2004-present
 NEWS  3  NOV 26     MARPAT enhanced with FSORT command
 NEWS  4  NOV 26     CHEMSAFE now available on STN Easy
 NEWS  5  NOV 26     Two new SET commands increase convenience of STN
                     searching
 NEWS  6  DEC 01     ChemPort single article sales feature unavailable
 NEWS  7  DEC 12     GBFULL now offers single source for full-text
                     coverage of complete UK patent families
 NEWS  8  DEC 17     Fifty-one pharmaceutical ingredients added to PS
 NEWS  9  JAN 06     The retention policy for unread STNmail messages
                     will change in 2009 for STN-Columbus and STN-Tokyo
 NEWS 10  JAN 07     WPIDS, WPINDEX, and WPIX enhanced Japanese Patent
                     Classification Data
 NEWS 11  FEB 02     Simultaneous left and right truncation (SLART) added
                     for CERAB, COMPUAB, ELCOM, and SOLIDSTATE
 NEWS 12  FEB 02     GENBANK enhanced with SET PLURALS and SET SPELLING
 NEWS 13  FEB 06     Patent sequence location (PSL) data added to USGENE
 NEWS 14  FEB 10     COMPENDEX reloaded and enhanced
 NEWS 15  FEB 11     WTEXTILES reloaded and enhanced
 NEWS 16  FEB 19     New patent-examiner citations in 300,000 CA/CAplus
                     patent records provide insights into related prior
                     art
 NEWS 17  FEB 19     Increase the precision of your patent queries -- use
                     terms from the IPC Thesaurus, Version 2009.01
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NEWS 18   FEB 23   Several formats for image display and print options
                   discontinued in USPATFULL and USPAT2
NEWS 19   FEB 23   MEDLINE now offers more precise author group fields
                   and 2009 MeSH terms
NEWS 20   FEB 23   TOXCENTER updates mirror those of MEDLINE - more
                   precise author group fields and 2009 MeSH terms
NEWS 21   FEB 23   Three million new patent records blast AEROSPACE into
                   STN patent clusters
NEWS 22   FEB 25   USGENE enhanced with patent family and legal status
                   display data from INPADOCDB
NEWS 23   MAR 06   INPADOCDB and INPAFAMDB enhanced with new display
                   formats
NEWS 24   MAR 11   EPFULL backfile enhanced with additional full-text
                   applications and grants
NEWS 25   MAR 11   ESBIOBASE reloaded and enhanced
NEWS 26   MAR 20   CAS databases on STN enhanced with new super role
                   for nanomaterial substances
NEWS 27   MAR 23   CA/CAplus enhanced with more than 250,000 patent
                   equivalents from China


NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
             AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.


NEWS HOURS     STN Operating Hours Plus Help Desk Availability
NEWS LOGIN     Welcome Banner and News Items
NEWS IPC8      For general information regarding STN implementation of IPC 8

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  and other penalties.

* * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 17:02:18 ON 29 MAR 2009

=> index bioscience
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS                              SINCE FILE      TOTAL
                                                    ENTRY        SESSION
FULL ESTIMATED COST                                 0.22          0.22


INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
       AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
       CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
       DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 17:02:31 ON 29 MAR 2009

68 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view
search error messages that display as 0* with SET DETAIL OFF.

=> s Lactobacillus reuteri and toxi? and CD+4(p)lymphocyte? and cultur?
          0*   FILE ADISNEWS
          0*   FILE ANTE
          0*   FILE AQUALINE
          0*   FILE BIOENG
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            0*  FILE BIOTECHABS
            0*  FILE BIOTECHDS
            0*  FILE BIOTECHNO
            0*  FILE CEABA-VTB
            0*  FILE CIN
   21 FILES SEARCHED...
            0*  FILE FOMAD
            0*  FILE FOREGE
            0*  FILE FROSTI
            0*  FILE FSTA
            0*  FILE KOSMET
   43 FILES SEARCHED...
            0*  FILE NTIS
            0*  FILE NUTRACEUT
            0*  FILE PASCAL
            0*  FILE PHARMAML
   61 FILES SEARCHED...
            0*  FILE WATER


    0 FILES HAVE ONE OR MORE ANSWERS,   68 FILES SEARCHED IN STNINDEX

L1   QUE LACTOBACILLUS REUTERI AND TOXI? AND CD+4(P) LYMPHOCYTE? AND CULTUR?


=> logoff
ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF
LOGOFF? (Y)/N/HOLD:y
COST IN U.S. DOLLARS                           SINCE FILE     TOTAL
                                                  ENTRY      SESSION
FULL ESTIMATED COST                               2.04        2.26

STN INTERNATIONAL LOGOFF AT 17:04:21 ON 29 MAR 2009




Connecting via Winsock to STN




Welcome to STN International!  Enter x:x

LOGINID:ssspt189dxw

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2


* * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1            Web Page for STN Seminar Schedule - N. America
 NEWS  2  APR 02    CAS Registry Number Crossover Limits Increased to
                    500,000 in Key STN Databases
 NEWS  3  APR 02    PATDPAFULL: Application and priority number formats
                    enhanced
 NEWS  4  APR 02    DWPI: New display format ALLSTR available
 NEWS  5  APR 02    New Thesaurus Added to Derwent Databases for Smooth
                    Sailing through U.S. Patent Codes
 NEWS  6  APR 02    EMBASE Adds Unique Records from MEDLINE, Expanding
                    Coverage back to 1948
 NEWS  7  APR 07    CA/CAplus CLASS Display Streamlined with Removal of
                    Pre-IPC 8 Data Fields
 NEWS  8  APR 07    50,000 World Traditional Medicine (WTM) Patents Now
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* * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 08:22:35 ON 01 OCT 2010

=> s Lactobacillus strain and immunomo? and ingest? and strain(p)select? and and
reuteri and CD4 and lymphocyt?
THIS COMMAND NOT AVAILABLE IN THE CURRENT FILE
Some commands only work in certain files. For example, the EXPAND
command can only be used to look at the index in a file which has an
index. Enter "HELP COMMANDS" at an arrow prompt (=>) for a list of
commands which can be used in this file.

=> index bioscience
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS   SINCE FILE   TOTAL
                                                     ENTRY   SESSION
FULL ESTIMATED COST   0.66   0.66

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,

62 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view
search error messages that display as 0* with SET DETAIL OFF.

=> s Lactobacillus strain and immunomo? and ingest? and strain(p)select? and and
reuteri and CD4 and lymphocyt?
MISSING TERM 'AND AND'
The search profile that was entered contains a logical
operator followed immediately by another operator.

=> s Lactobacillus and strain and immunomo? and ingest? and strain(p)select? and
and reuteri and CD4 and lymphocyt?
MISSING TERM 'AND AND'
The search profile that was entered contains a logical
operator followed immediately by another operator.

=> s Lactobacillus strain and immunomo? and ingest? and strain(p)select? and
reuteri and CD4 and lymphocyt?
          0* FILE ADISNEWS
          0* FILE ANTE
          0* FILE AQUALINE
   8 FILES SEARCHED...
          0* FILE BIOENG
          0* FILE BIOTECHABS
          0* FILE BIOTECHDS
          0* FILE BIOTECHNO
  14 FILES SEARCHED...
          0* FILE CEABA-VTB
          0* FILE CIN
  21 FILES SEARCHED...
  23 FILES SEARCHED...
  30 FILES SEARCHED...
          0* FILE FOMAD
          0* FILE FROSTI
          0* FILE FSTA
  38 FILES SEARCHED...
          0* FILE KOSMET
          0* FILE NTIS
          0* FILE PASCAL
  54 FILES SEARCHED...
          5   FILE USPATFULL
          0* FILE WATER

   1 FILES HAVE ONE OR MORE ANSWERS,   62 FILES SEARCHED IN STNINDEX

L1   QUE LACTOBACILLUS STRAIN AND IMMUNOMO? AND INGEST? AND STRAIN(P)SELECT? AN
        D REUTERI AND CD4 AND LYMPHOCYT?

=> file uspatfull
COST IN U.S. DOLLARS   SINCE FILE   TOTAL
                                                    ENTRY   SESSION
FULL ESTIMATED COST   4.83   5.49

FILE 'USPATFULL' ENTERED AT 08:27:56 ON 01 OCT 2010
CA INDEXING COPYRIGHT (C) 2010 AMERICAN CHEMICAL SOCIETY (ACS)

FILE COVERS 1971 TO PATENT PUBLICATION DATE: 30 Sep 2010 (20100930/PD)

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=> s l1
            9865 LACTOBACILLUS
          298249 STRAIN
             291 LACTOBACILLUS STRAIN
                    (LACTOBACILLUS(W)STRAIN)
           23060 IMMUNOMO?
           69968 INGEST?
          298249 STRAIN
         3641712 SELECT?
           59013 STRAIN(P)SELECT?
             793 REUTERI
           34062 CD4
           90915 LYMPHOCYT?
L2             5 LACTOBACILLUS STRAIN AND IMMUNOMO? AND INGEST? AND STRAIN(P)SELE
                 CT? AND REUTERI AND CD4 AND LYMPHOCYT?


=> dup rem l2
PROCESSING COMPLETED FOR L2
L3             5 DUP REM L2 (0 DUPLICATES REMOVED)


=> d l3 1-5


L3   ANSWER 1 OF 5  USPATFULL on STN
AN      2010:145673  USPATFULL
TI      Stabilized bacterial formulation
IN      Bjorksten, Bengt, Stockholm, SWEDEN
        Mollstam, Bo, Lerum, SWEDEN
PI      US 20100129336     A1  20100527
AI      US 2009-590313     A1  20091105 (12)
RLI     Division of Ser. No. US 2004-860201, filed on 3 Jun 2004, PENDING
DT      Utility
FS      APPLICATION
LN.CNT 715
INCL    INCLM: 424/093.450
        INCLS: 435/252.900
NCL     NCLM:  424/093.450
        NCLS:  435/252.900
IC      IPCI   A61K0045-00 [I,A]; C12N0001-20 [I,A]; A61P0043-00 [I,A]


L3   ANSWER 2 OF 5  USPATFULL on STN
AN      2009:151614  USPATFULL
TI      Anti-inflammatory activity from lactic acid bacteria
IN      Versalovic, James, Houston, TX, UNITED STATES
        Pena, Jeremy A., Houston, TX, UNITED STATES
        Connolly, Ramonn, Lidingo, SWEDEN
PI      US 20090136454     A1  20090528
AI      US 2008-69050      A1  20080207 (12)
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RLI     Division of Ser. No. US 2004-767317, filed on 29 Jan 2004, ABANDONED
PRAI    US 2003-443644P          20030130 (60)
DT      Utility
FS      APPLICATION
LN.CNT 2076
INCL    INCLM: 424/093.400
NCL     NCLM:  424/093.400
IC      IPCI   A61K0035-74 [I,A]; A61K0035-66 [I,C*]
        IPCR   A61K0035-66 [I,C]; A61K0035-74 [I,A]; A61K [I,S]; A61K0006-00
               [I,C*]; A61K0006-00 [I,A]; A61K0035-00 [I,C*]; A61K0035-00 [I,A];
               A61K0038-17 [I,C*]; A61K0038-17 [I,A]; C07K0014-195 [I,C*];
               C07K0014-335 [I,A]; C12N0001-20 [I,C*]; C12N0001-20 [I,A];
               C12R0001-225 [N,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3      ANSWER 3 OF 5   USPATFULL on STN
AN      2008:289979   USPATFULL
TI      Use of selected lactic acid bacteria for reducing atherosclerosis
IN      Rothschild, Peter, Lidingo, SWEDEN
        Connolly, Eamonn, Lidingo, SWEDEN
        Mollstam, Bo, Lerum, SWEDEN
PI      US 20080254011     A1  20081016
AI      US 2007-786356     A1  20070411 (11)
DT      Utility
FS      APPLICATION
LN.CNT 923
INCL    INCLM: 424/093.450
        INCLS: 426/061.000; 435/252.100
NCL     NCLM:  424/093.450
        NCLS:  426/061.000; 435/252.100
IC      IPCI   A61K0035-74 [I,A]; A61K0035-66 [I,C*]; A23C0009-12 [I,A];
               A61P0009-10 [I,A]; A61P0009-00 [I,C*]; C12N0001-20 [I,A]
        IPCR   A61K0035-66 [I,C]; A61K0035-74 [I,A]; A23C0009-12 [I,C];
               A23C0009-12 [I,A]; A61P0009-00 [I,C]; A61P0009-10 [I,A];
               C12N0001-20 [I,C]; C12N0001-20 [I,A]

L3      ANSWER 4 OF 5   USPATFULL on STN
AN      2005:312024   USPATFULL
TI      Method for improved breast milk feeding to reduce the risk of allergy
IN      Bjorksten, Bengt, Stockholm, SWEDEN
        Mollstam, Bo, Lerum, SWEDEN
        Sjoberg, Elisabeth, Lund, SWEDEN
PI      US 20050271641     A1  20051208
AI      US 2004-860201     A1  20040603 (10)
DT      Utility
FS      APPLICATION
LN.CNT 703
INCL    INCLM: 424/093.450
NCL     NCLM:  424/093.450
IPC     [7]
        IPCI   A61K0045-00 [ICM,7]
        IPCR   A61K0035-66 [I,C*]; A61K0035-74 [I,A]; A61K0045-00 [I,C*];
               A61K0045-00 [I,A]; C12Q0001-02 [I,C*]; C12Q0001-02 [I,A];
               G01N0033-68 [I,C*]; G01N0033-68 [I,A]

L3      ANSWER 5 OF 5   USPATFULL on STN
AN      2005:117266   USPATFULL
TI      Probiotic therapies
IN      Bienenstock, John, Toronto, CANADA
PI      US 20050100531     A1  20050512
AI      US 2004-8232       A1  20041210 (11)
RLI     Continuation of Ser. No. WO 2003-IE90, filed on 13 Jun 2003, UNKNOWN
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PRAI   IE 2002-479              20020613
DT     Utility
FS     APPLICATION
LN.CNT 1048
INCL   INCLM: 424/093.200
       INCLS: 514/044.000; 435/252.300
NCL    NCLM:  424/093.200
       NCLS:  435/252.300; 514/044.000R
IPC    [7]
       IPCI   A61K0048-00 [ICM,7]; C12N0001-21 [ICS,7]
       IPCR   A61K0035-66 [I,C*]; A61K0035-74 [I,A]; A61K0038-18 [I,C*];
              A61K0038-18 [I,A]


=> d hist

       (FILE 'HOME' ENTERED AT 08:22:35 ON 01 OCT 2010)

       INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
       AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
       CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
       DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 08:24:15 ON 01 OCT 2010
                        SEA LACTOBACILLUS STRAIN AND IMMUNOMO? AND INGEST? AND STRAIN(P
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                        0*   FILE ADISNEWS
                        0*   FILE ANTE
                        0*   FILE AQUALINE
                        0*   FILE BIOENG
                        0*   FILE BIOTECHABS
                        0*   FILE BIOTECHDS
                        0*   FILE BIOTECHNO
                        0*   FILE CEABA-VTB
                        0*   FILE CIN
                        0*   FILE FOMAD
                        0*   FILE FROSTI
                        0*   FILE FSTA
                        0*   FILE KOSMET
                        0*   FILE NTIS
                        0*   FILE PASCAL
                        5    FILE USPATFULL
                        0*   FILE WATER
L1                        QUE LACTOBACILLUS STRAIN AND IMMUNOMO? AND INGEST? AND STRAIN(P
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       FILE 'USPATFULL' ENTERED AT 08:27:56 ON 01 OCT 2010
L2             5 S L1
L3             5 DUP REM L2 (0 DUPLICATES REMOVED)

=> s l3 and CD4
L4            5 S L3
         34062 CD4
L5            5 L4 AND CD4

=> d l3 5 ab

L3   ANSWER 5 OF 5  USPATFULL on STN
AB      Use of a bacterial strain or an active derivative, fragment or
        mutant thereof which selectively upregulates the production of
        nerve growth factor (NGF), brain derived neurotrophic factor (BDNF),
        neurotrophin 3 (NT3) or neurotrophin 4 (NT4) in the treatment and/or
        prophylaxis of various disorders especially inflammatory disorders. The
        bacterial strain may be a Lactobacillus
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          especially,Lactobacillus reuteri.


=> d l3 5 kwic

L3    ANSWER 5 OF 5  USPATFULL on STN
AB       Use of a bacterial strain or an active derivative, fragment or
         mutant thereof which selectively upregulates the production of
         nerve growth factor (NGF), brain derived neurotrophic factor (BDNF),
         neurotrophin 3 (NT3) or neurotrophin 4 (NT4) in the treatment and/or
         prophylaxis of various disorders especially inflammatory disorders. The
         bacterial strain may be a Lactobacillus
         especially,Lactobacillus reuteri.
SUMM     .  .  . M. E. Lamm. Ann. Rev. Microbiol. 1997, 51, 311). In addition,
         antigen presentation may occur via epithelial cells to intraepithelial
         lymphocytes and to the underlying lamina propria immune cells
         (S. Raychaudhuri et al. Nat Biotechnol., 1998, 16, 1025). Therefore, the
         host.  .  . significant damage to the host. In fact, the intestinal
         flora contributes to defence of the host by competing with newly
         ingested potentially pathogenic micro-organisms.
SUMM      According to the invention there is provided use of a bacterial
         strain or an active derivative, fragment or mutant thereof which
         selectively upregulates the production of nerve growth factor
         (NGF), brain derived neurotrophic factor (BDNF), neurotrophin 3 (NT3) or
         neurotrophin 4 (NT4).  .  .
SUMM      In one embodiment of the invention the bacterial strain is a
         Lactobacillus. Preferably the Lactobacillus is Lactobacillus
         reuteri.
SUMM      The invention provides use of a bacterial strain or an active
         derivative, fragment or mutant thereof which selectively
         upregulates the production of NGF, BDNF, NT3 or NT4 in the treatment
         and/or prophylaxis of various diseases such as inflammatory.  .  .
SUMM      The invention further provides use of a bacterial strain or
         an active derivative, fragment or mutant thereof which
         selectively upregulates the production of NGF, BDNF, NT3 or NT4
         and IL-10 in the treatment and/or prophylaxis of inflammatory disorders,
         immunodeficiency,.  .  .
SUMM      The invention further provides a vaccine comprising a bacterial
         strain or an active derivative, fragment or mutant thereof which
         selectively upregulates the production of NGF, BDNF, NT3 or NT4
         in the treatment and/or prophylaxis of inflammatory disorders,
         immunodeficiency, inflammatory bowel.  .  .
SUMM      The invention also provides a vaccine comprising a bacterial
         strain or an active derivative, fragment or mutant thereof which
         selectively upregulates the production of NGF, BDNF, NT3 or NT4
         in the treatment and/or prophylaxis of various diseases such as
         inflammatory.  .  .
DRWD      FIG. 5 is a bar graph showing the inhibitory effect of a
         lactobacillus strain on TNFα induced IL-8 mRNA
         levels; and
DRWD      FIG. 6 is a bar graph showing the inhibitory effect of a
         lactobacillus strain on TNFα induced IL-8
         protein levels.
DETD      .  .  . in the present invention that particular strains of commensal
         micro-organisms such as Bifidobacteria and Lactobacilli, induced NGF
         synthesis resulting in immunomodulatory effects in vitro.
DETD      It was surprisingly found in the present invention that on stimulation
         of epithelial cells with Lactobacillus reuteri NGF was
         selectively induced resulting in the attenuation of TNF induced IL-8
         cytokine production.
DETD      Lactobacillus is commercially available. Lactobacillus reuteri
         strain type RF 14249 and RF 20013 is deposited under the designation
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F275 (DSM20016), JCM112, ATCC23272, NCD02589.

DETD   . . . the nervous system: these include structural cells such as the glia, and fibroblasts, cells of the immune system such as T-lymphocytes (especially TH2) and cells involved in the inflammatory process such as eosinophils, mast cells and dendritic cells. It has pleiotropic. . .

DETD   Other Bifidobacteria and Lactobacilli strains potentially have the same effect as L. reuteri. Such Bifidobacteria and Lactobacilli are typically isolated from the microbial flora within the human gastrointestinal tract. The immune system within. . .

DETD   . . . host to react to non-pathogenic, but antigenic, agents resulting in allergy or autoimmunity. Deliberate consumption of a series of non-pathogenic immunomodulatory bacteria would provide the host with the necessary and appropriate educational stimuli for proper development and control of immune function.

DETD   . . . The activity of a number of cell types can be suppressed by TGFβ including natural killer (NK) cells, cytotoxic T lymphocytes and lymphokine activated killer (LAK) cells. TGFβ also has suppressive effects on the release of reactive oxygen and nitrogen intermediates. . .

DETD   . . . by certain pathogenic bacteria or proinflammatory cytokines, such as TNF, results in the release of IL-8 which recruits neutrophils and lymphocytes to damaged or inflamed sites. Roles other than chemotaxis have been described for some of these family members. MCP-1 stimulates. . .

DETD   . . . seen during an inflammatory response. This cytokine is primarily a monocyte or macrophage derived product but other cell types including lymphocytes, neutrophils, NK cells, mast cells, astrocytes, epithelial cells (Neale et al., 1995) endothelial cells and smooth muscle cells can also. . .

DETD   The introduction of probiotic organisms is accomplished by the ingestion of the micro-organism in a suitable carrier. It would be advantageous to provide a medium that would promote the growth. . .

DETD   Human colonic epithelial cell lines T-84 and HT-29 were co-incubated with Lactobacillus reuteri for 2 hours. IL-6, IL-8, IL-10, and NGF mRNA levels were quantified using RT-PCR. L. reuteri selectively increased NGF levels (FIG. 4). None of the other cytokines were induced by bacterial stimulation.

DETD   Human colonic epithelial cell lines T-84 and HT-29 were co-incubated with Lactobacillus reuteri for 2 hours, followed by 30 minutes incubation with 10 ng/ml TNFα. IL-8 mRNA levels were quantified using RT-PCR. In. . . measured following co-incubation with brefeldin A for 3 hours. Cells were then lysed and IL-8 levels quantified by ELISA. L. reuteri attenuated TNF induced IL-8 production both at the mRNA and protein level (FIGS. 5 & 6). Heat inactivated bacterial cells did not maintain this immunomodulatory effect (FIG. 5).

DETD   . . . M, Fazekas de St Groth B. The presence of interleukin 4 during in vitro priming determines the lymphokine-producing potential of CD4+ T cells from T cell receptor transgenic mice. J Exp Med 1992 Oct 1;176(4):1091-8.

Mosmann T. R. & Sad. . . more. Immunol. Today, 1996; 17:138-46.

Trinchieri G, Peritt D, Gerosa F. Acute induction and priming for cytokine production in lymphocytes. Cytokine Growth Factor Rev 1996 Aug;7(2):123-32.

Maldonado-Lopez R. De Smedt T., Michel P., Godfroid J., Pajak B., Heirman C.,. . .

Groux H., O'Garra A., Bigler M., Rouleau M., Antonenko S., de Vries J. E. & Roncarolo M. G. A CD4+ T-cell subset inhibits antigen-specific T-cell responses and prevents colitis. Nature, 1997; 389:737-42.

Jonuleit H., Schmitt E., Schuler G., Knop J. & EnK A. H. Induction of interleukin 10-producing, nonproliferating CD4+ T cells with regulatory properties by repetitive stimulation with allogeneic immature

human dendritic cells. J. Exp. Med., 2000; 192:1213-22.
. . . prostaglandin-dependent matrix metalloproteinase production. J Biol
    Chem 1994 Aug 19;269(33):21322-9. Ma X, Aste-Amezaga M, Gri G, Gerosa F,
    Triochieri G. Immunomodulatory functions and molecular
    regulation of IL-12. Chem Immunol 1997;68:1-22.
 Schmitt E, Rude E, Germann T. The immunostimulatory function of. . .
CLM   What is claimed is:
. . . system, hepatic disease, ischaemia, nutritional disorders,
    osteoporosis, endocrine disorders, epidermal disorders, psoriasis and/or
    acne vulgaris comprising use of a bacterial strain or an
    active derivative, fragment or mutant thereof which selectively
    upregulates the production of nerve growth factor (NGF), brain derived
    neurotrophic factor (BDNF), neurotrophin 3 (NT3) or neurotrophin 4
    (NT4).
        . . .
CLM   What is claimed is:
    4. A method as claimed in claim 3 wherein the Lactobacillus is a
    Lactobacillus reuteri.

CLM   What is claimed is:
    6. A method for the treatment and/or prophylaxis of various diseases
    such as inflammatory diseases comprising use of a bacterial
    strain or an active derivative, fragment or mutant thereof which
    selectively upregulates the production of NGF.

CLM   What is claimed is:
. . . system, hepatic disease, ischaemia, nutritional disorders,
    osteoporosis, endocrine disorders, epidermal disorders, psoriasis and/or
    acne vulgaris comprising use of a bacterial strain or an
    active derivative, fragment or mutant thereof which selectively
    upregulates the production of NGF, BDNF, NT3 or NT4 and IL-10.

CLM   What is claimed is:
    16. A vaccine comprising a bacterial strain or an active
    derivative, fragment or mutant thereof which selectively
    upregulates the production of NGF, BDNF, NT3 or NT4 in the treatment
    and/or prophylaxis of inflammatory disorders, immunodeficiency,
    inflammatory bowel. . .
CLM   What is claimed is:
    17. A vaccine comprising a bacterial strain or an active
    derivative, fragment or mutant thereof which selectively
    upregulates the production of NGF, BDNF, NT3 or NT4 in the treatment
    and/or prophylaxis of various diseases such as inflammatory. . .

=> d l5 1-5

L5   ANSWER 1 OF 5 USPATFULL on STN
AN   2010:145673 USPATFULL
TI   Stabilized bacterial formulation
IN   Bjorksten, Bengt, Stockholm, SWEDEN
        Mollstam, Bo, Lerum, SWEDEN
PI   US 20100129336   A1 20100527
AI   US 2009-590313   A1 20091105 (12)
RLI   Division of Ser. No. US 2004-860201, filed on 3 Jun 2004, PENDING
DT   Utility
FS   APPLICATION
LN.CNT 715
INCL   INCLM: 424/093.450
        INCLS: 435/252.900
NCL   NCLM: 424/093.450
        NCLS: 435/252.900

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IC      IPCI    A61K0045-00 [I,A]; C12N0001-20 [I,A]; A61P0043-00 [I,A]

L5   ANSWER 2 OF 5  USPATFULL on STN
AN      2009:151614  USPATFULL
TI      Anti-inflammatory activity from lactic acid bacteria
IN      Versalovic, James, Houston, TX, UNITED STATES
        Pena, Jeremy A., Houston, TX, UNITED STATES
        Connolly, Ramonn, Lidingo, SWEDEN
PI      US 20090136454     A1  20090528
AI      US 2008-69050      A1  20080207 (12)
RLI     Division of Ser. No. US 2004-767317, filed on 29 Jan 2004, ABANDONED
PRAI    US 2003-443644P         20030130 (60)
DT      Utility
FS      APPLICATION
LN.CNT 2076
INCL    INCLM: 424/093.400
NCL     NCLM:  424/093.400
IC      IPCI    A61K0035-74 [I,A]; A61K0035-66 [I,C*]
        IPCR    A61K0035-66 [I,C]; A61K0035-74 [I,A]; A61K [I,S]; A61K0006-00
                [I,C*]; A61K0006-00 [I,A]; A61K0035-00 [I,C*]; A61K0035-00 [I,A];
                A61K0038-17 [I,C*]; A61K0038-17 [I,A]; C07K0014-195 [I,C*];
                C07K0014-335 [I,A]; C12N0001-20 [I,C*]; C12N0001-20 [I,A];
                C12R0001-225 [N,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5   ANSWER 3 OF 5  USPATFULL on STN
AN      2008:289979  USPATFULL
TI      Use of selected lactic acid bacteria for reducing atherosclerosis
IN      Rothschild, Peter, Lidingo, SWEDEN
        Connolly, Eamonn, Lidingo, SWEDEN
        Mollstam, Bo, Lerum, SWEDEN
PI      US 20080254011     A1  20081016
AI      US 2007-786356     A1  20070411 (11)
DT      Utility
FS      APPLICATION
LN.CNT 923
INCL    INCLM: 424/093.450
        INCLS: 426/061.000; 435/252.100
NCL     NCLM:  424/093.450
        NCLS:  426/061.000; 435/252.100
IC      IPCI    A61K0035-74 [I,A]; A61K0035-66 [I,C*]; A23C0009-12 [I,A];
                A61P0009-10 [I,A]; A61P0009-00 [I,C*]; C12N0001-20 [I,A]
        IPCR    A61K0035-66 [I,C]; A61K0035-74 [I,A]; A23C0009-12 [I,C];
                A23C0009-12 [I,A]; A61P0009-00 [I,C]; A61P0009-10 [I,A];
                C12N0001-20 [I,C]; C12N0001-20 [I,A]

L5   ANSWER 4 OF 5  USPATFULL on STN
AN      2005:312024  USPATFULL
TI      Method for improved breast milk feeding to reduce the risk of allergy
IN      Bjorksten, Bengt, Stockholm, SWEDEN
        Mollstam, Bo, Lerum, SWEDEN
        Sjoberg, Elisabeth, Lund, SWEDEN
PI      US 20050271641     A1  20051208
AI      US 2004-860201     A1  20040603 (10)
DT      Utility
FS      APPLICATION
LN.CNT 703
INCL    INCLM: 424/093.450
NCL     NCLM:  424/093.450
IPC     [7]
        IPCI    A61K0045-00 [ICM,7]
        IPCR    A61K0035-66 [I,C*]; A61K0035-74 [I,A]; A61K0045-00 [I,C*];
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                A61K0045-00 [I,A]; C12Q0001-02 [I,C*]; C12Q0001-02 [I,A];
                G01N0033-68 [I,C*]; G01N0033-68 [I,A]

L5   ANSWER 5 OF 5  USPATFULL on STN
AN      2005:117266  USPATFULL
TI      Probiotic therapies
IN      Bienenstock, John, Toronto, CANADA
PI      US 20050100531      A1  20050512
AI      US 2004-8232        A1  20041210 (11)
RLI     Continuation of Ser. No. WO 2003-IE90, filed on 13 Jun 2003, UNKNOWN
PRAI    IE 2002-479              20020613
DT      Utility
FS      APPLICATION
LN.CNT 1048
INCL    INCLM: 424/093.200
        INCLS: 514/044.000; 435/252.300
NCL     NCLM:  424/093.200
        NCLS:  435/252.300; 514/044.000R
IPC     [7]
        IPCI   A61K0048-00 [ICM,7]; C12N0001-21 [ICS,7]
        IPCR   A61K0035-66 [I,C*]; A61K0035-74 [I,A]; A61K0038-18 [I,C*];
               A61K0038-18 [I,A]


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        (FILE 'HOME' ENTERED AT 08:22:35 ON 01 OCT 2010)

        INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
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        CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
        DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 08:24:15 ON 01 OCT 2010
                SEA LACTOBACILLUS STRAIN AND IMMUNOMO? AND INGEST? AND STRAIN(P
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                0*  FILE ADISNEWS
                0*  FILE ANTE
                0*  FILE AQUALINE
                0*  FILE BIOENG
                0*  FILE BIOTECHABS
                0*  FILE BIOTECHDS
                0*  FILE BIOTECHNO
                0*  FILE CEABA-VTB
                0*  FILE CIN
                0*  FILE FOMAD
                0*  FILE FROSTI
                0*  FILE FSTA
                0*  FILE KOSMET
                0*  FILE NTIS
                0*  FILE PASCAL
                5   FILE USPATFULL
                0*  FILE WATER
L1               QUE LACTOBACILLUS STRAIN AND IMMUNOMO? AND INGEST? AND STRAIN(P
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        FILE 'USPATFULL' ENTERED AT 08:27:56 ON 01 OCT 2010
L2              5 S L1
L3              5 DUP REM L2 (0 DUPLICATES REMOVED)
L4              5 S L3
L5              5 S L3 AND CD4


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ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF
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COST IN U.S. DOLLARS                          SINCE FILE      TOTAL
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